

FIG. 1

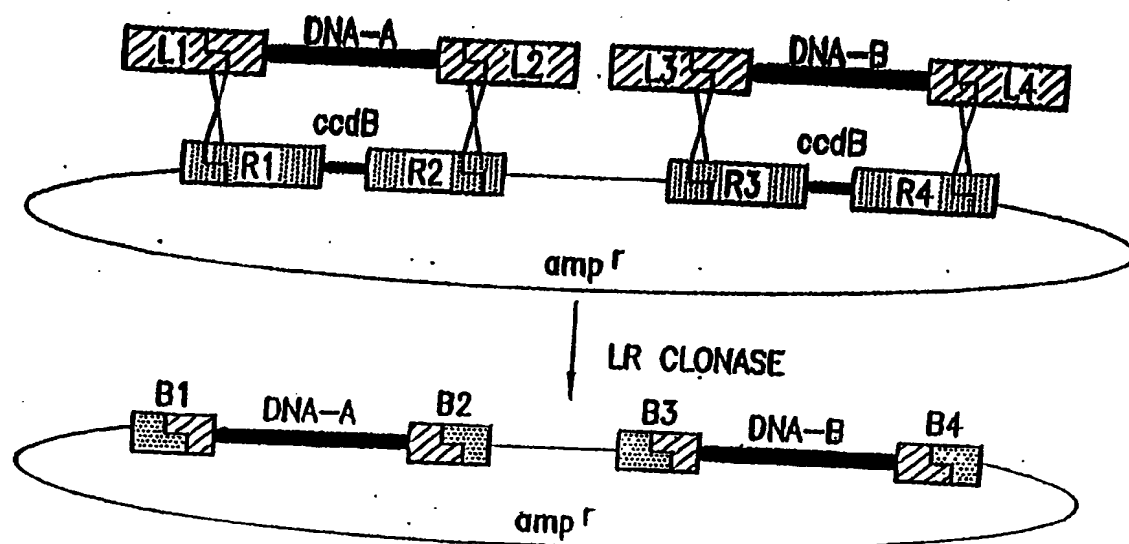


FIG. 2

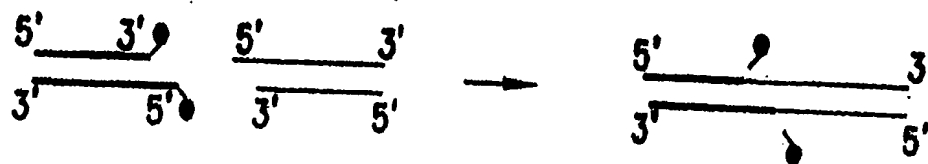


FIG. 3A

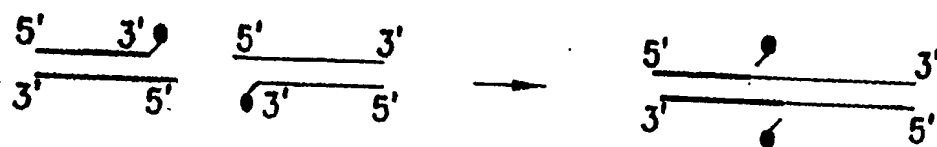


FIG. 3B

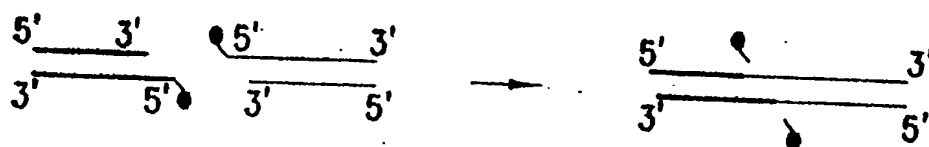


FIG. 3C

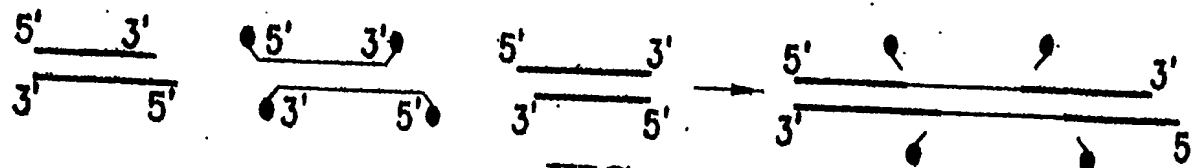
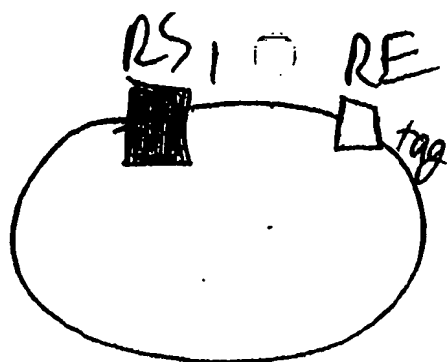
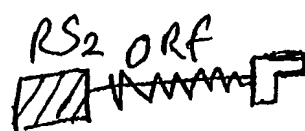
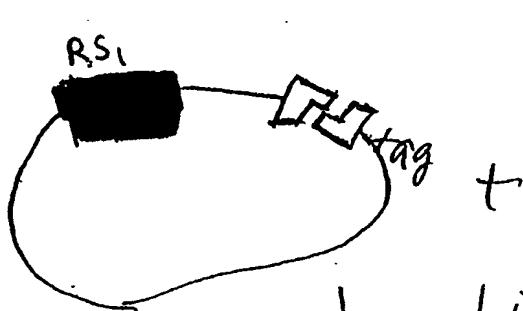


FIG. 3D



↓ RE Digest



Ligase + Recombination proteins

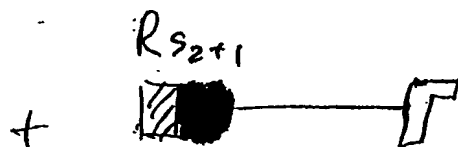
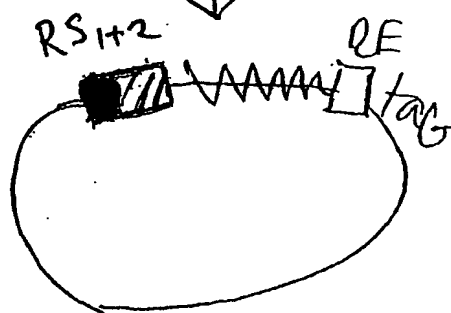


Fig. 4

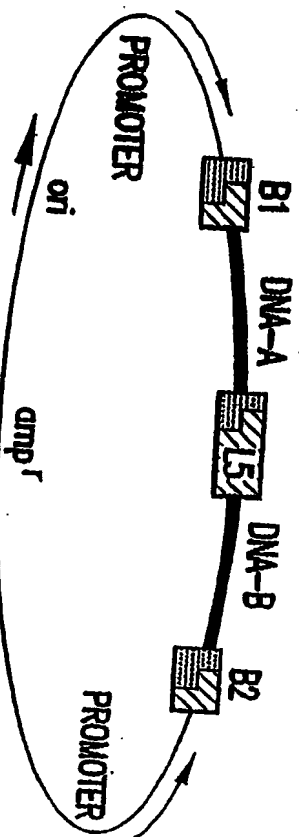


FIG. 5A

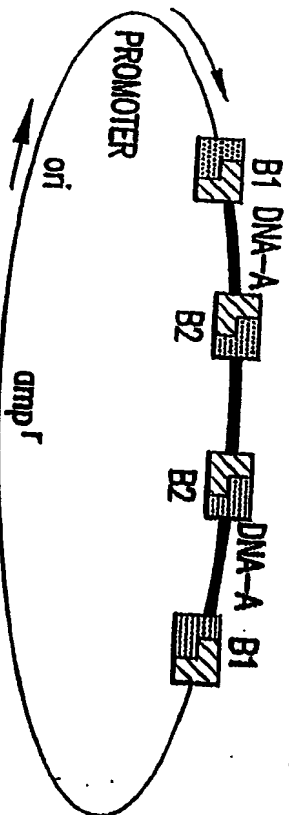


FIG. 5D

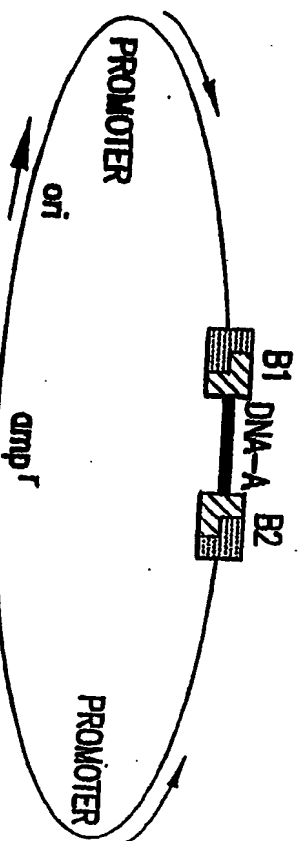


FIG. 5B

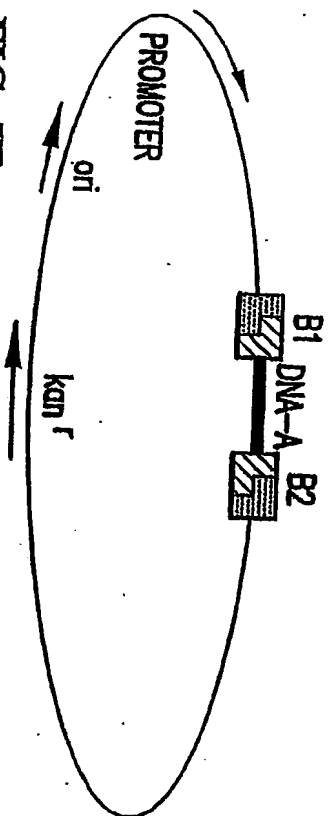


FIG. 5E

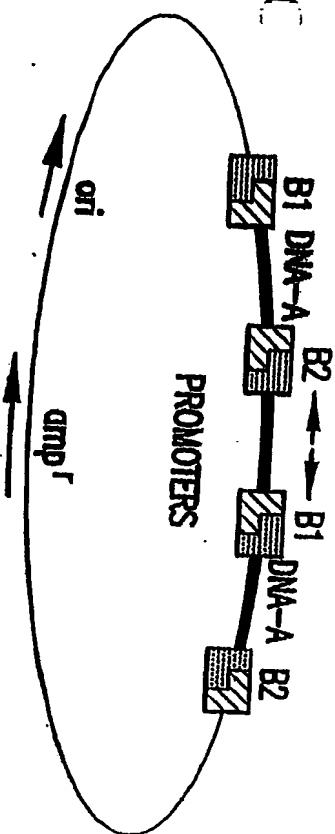


FIG. 5C

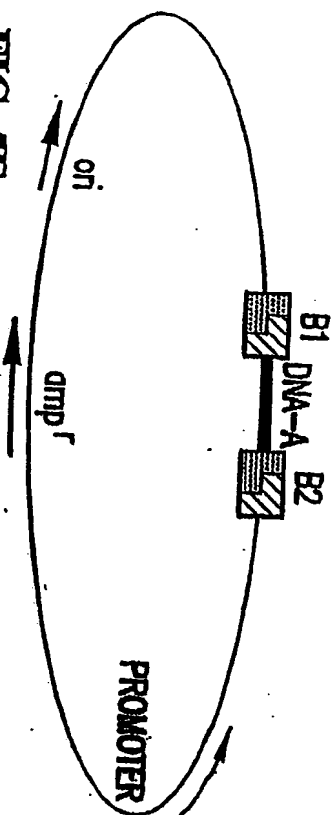


FIG. 5F

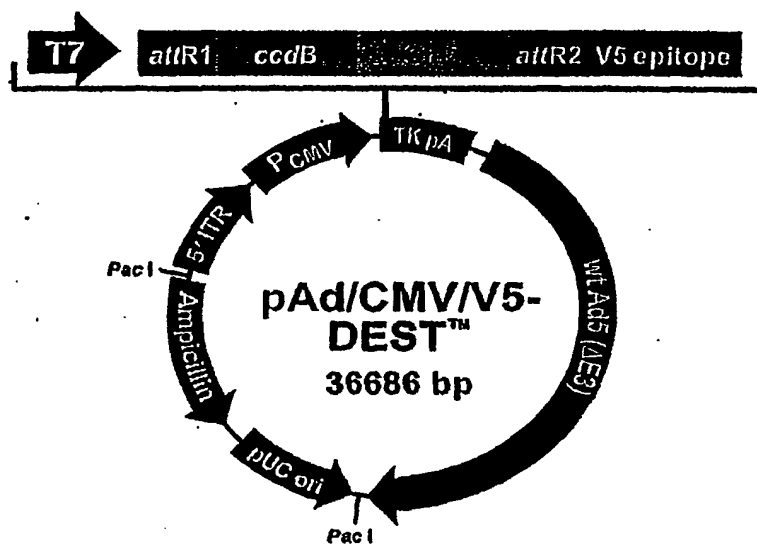


FIG. 6

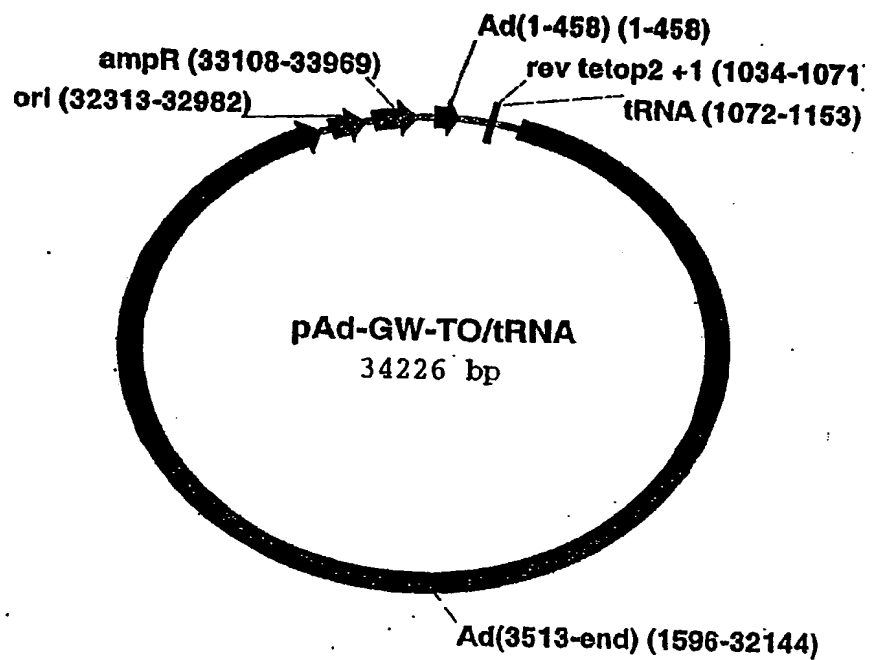


FIG. 7

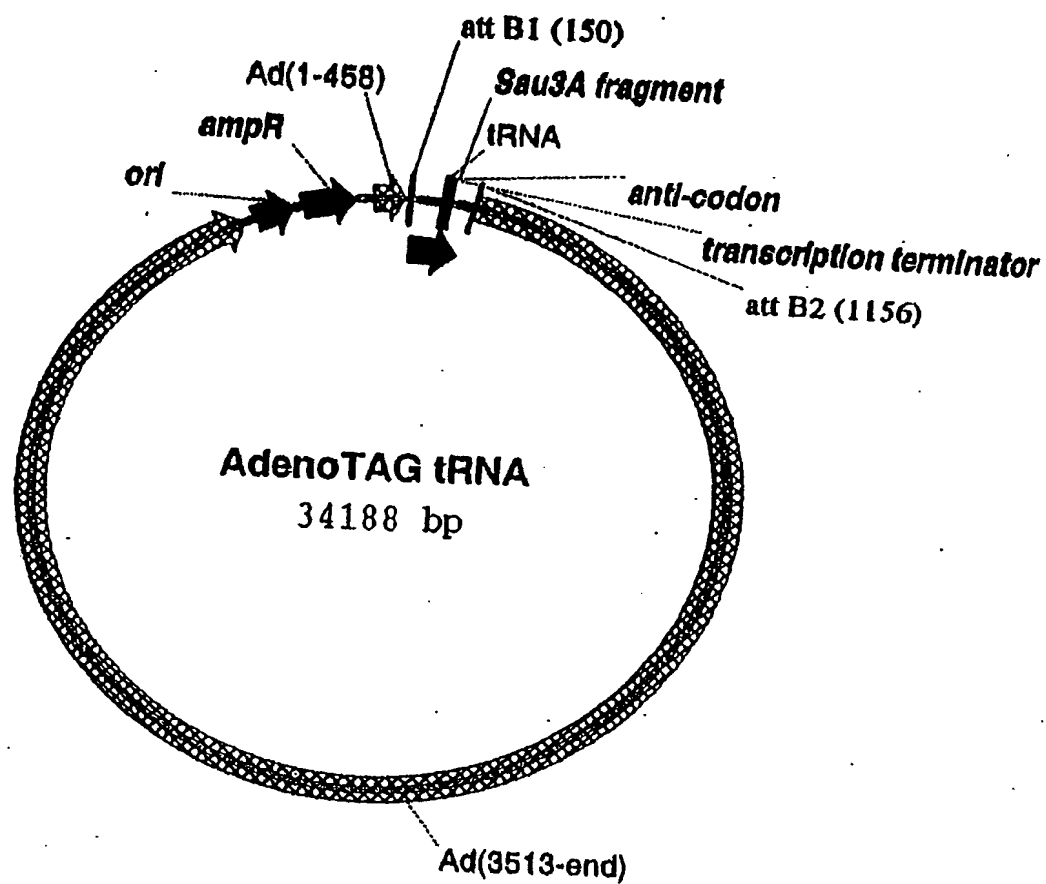


FIG. 8

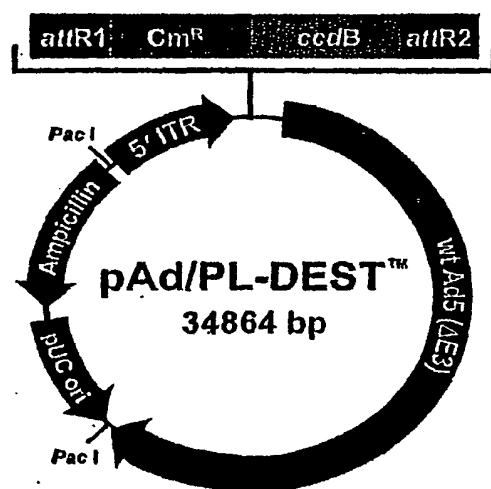


FIG. 9

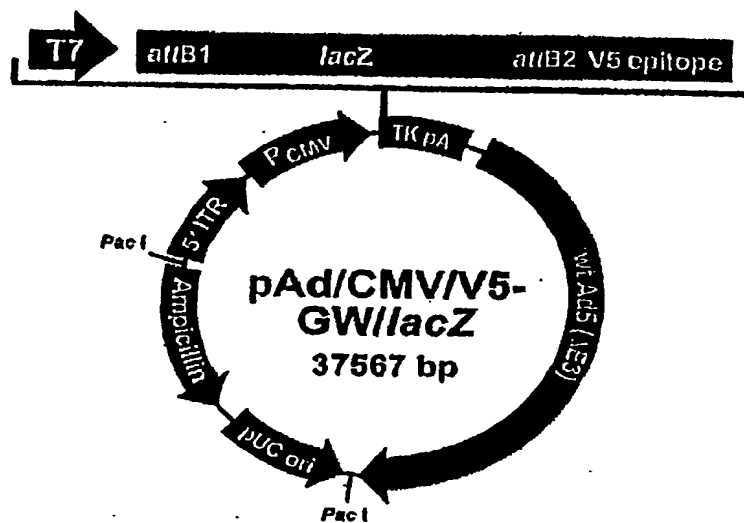


FIG. 10

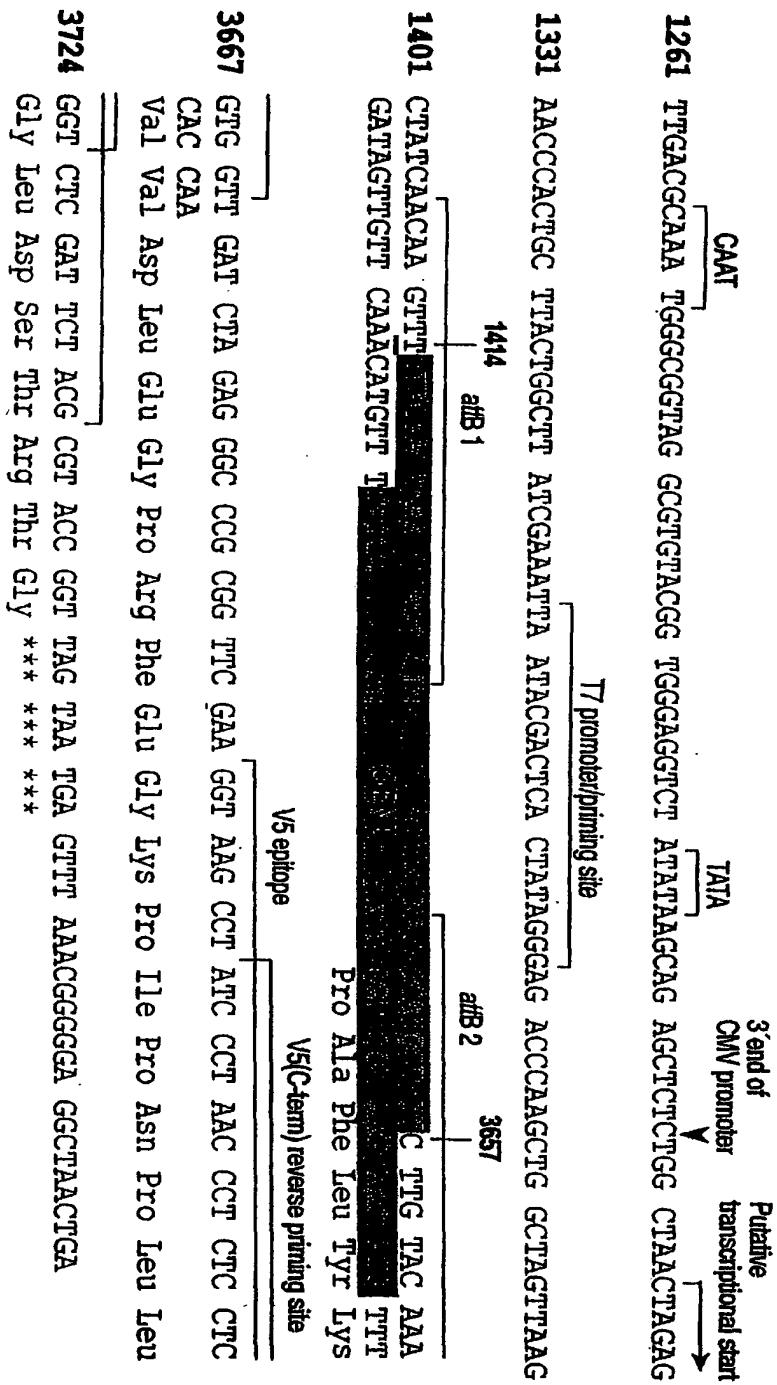


FIG. 11

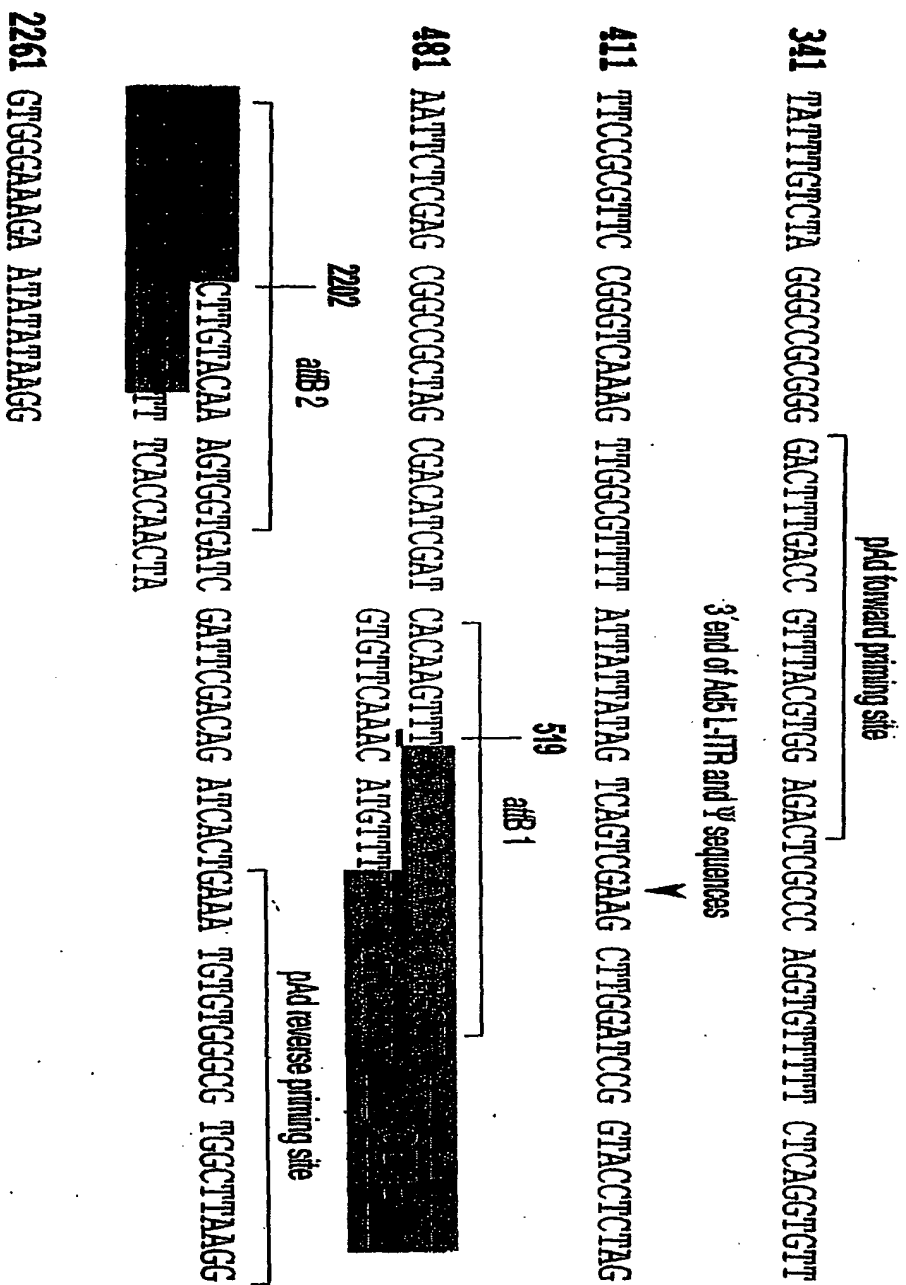


FIG. 12

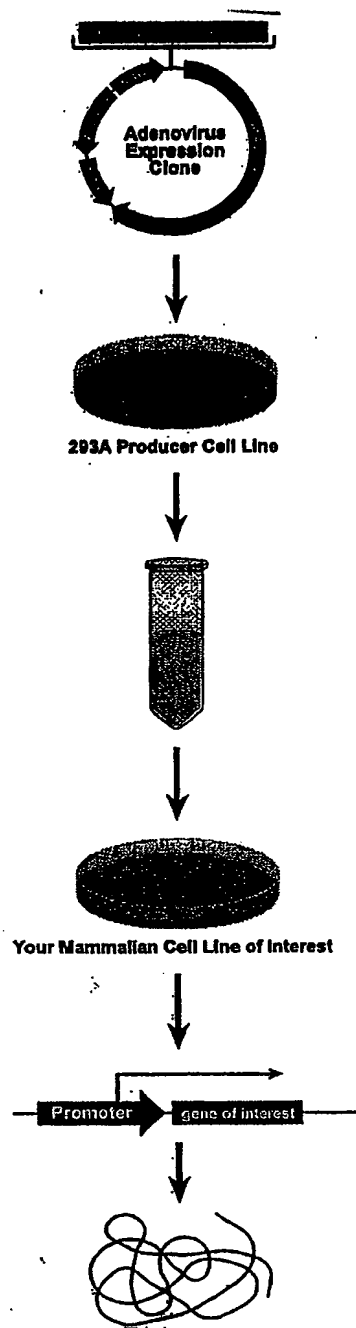


FIG. 13

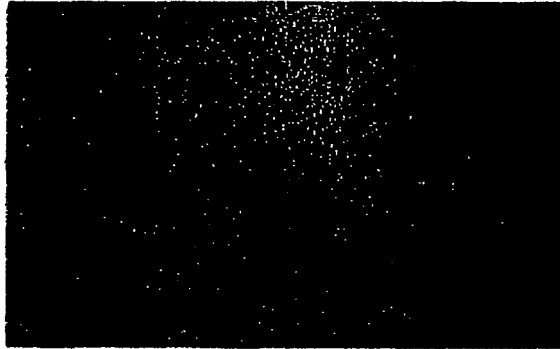


FIG. 14A

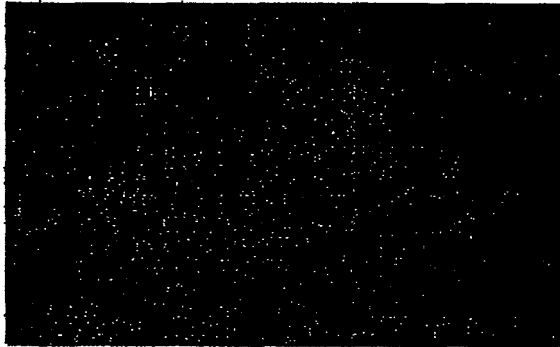


FIG. 14B

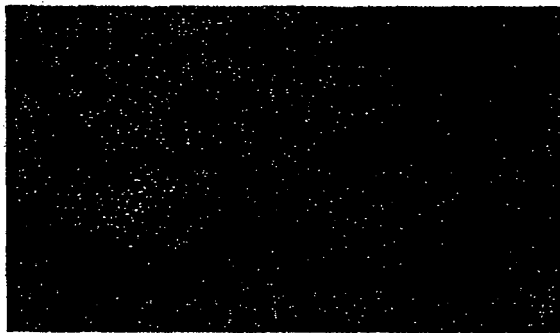


FIG. 14C

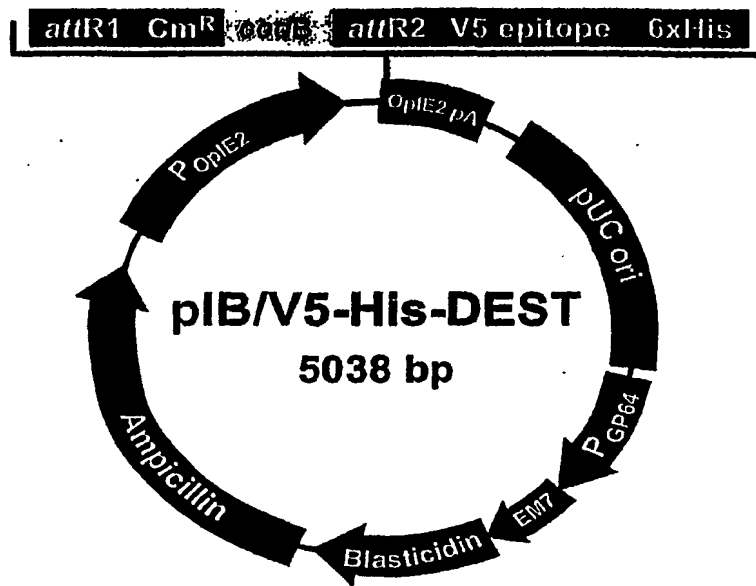


FIG. 15

1 GGATCATGAT GATAAACAAT GTATGGTGCT AATGTTGCTT CAACAACAAT TCTGTTGAAC
61 TGTGTTTCA TGTGTGCCAA CAAGCACCTT TATACTCGGT GGCCTCCCCA CCACCAACTT
121 TTTTGCACTG CAAAAAACA CGCTTTTGCA CGCGGGCCCA TACATAGTAC AAACCTCTAG
181 TTTCTAGAC TATTTTACAT AAATAGTCTA CACCGTTGTA TACGCTCCAA ATACACTACC
241 ACACATTGAA CCTTTTGCA GTGCAAAAAA GTACGTGTCTG GCAGTCACGT AGGCCGGCCT
301 TATCGGGTCTG CGTCCTGTCA CGTACGAATC ACATTATCGG ACCGGACGAG TGTGTCTTA
361 TCGTGACAGG ACGCCAGCTT CCTGTGTTGC TAACCGCAGC CGGACGCAAC TCCTTATCGG
421 AACAGGACGC GCCTCCATAT CAGCCGCGCG TTATCTCATG CGCGTGACCG GACACGAGGC
481 GCCCGTCCCG CTTATCGCGC CTATAAATAC AGCCCGCAAC GATCTGGTAA ACACAGTTGA
541 ACAGCATCTG TTCGAATTTA

TATA
Start of Transcription

FIG. 16

TATA Box
Start of transcription
OplE2 Forward priming site

487 CTTATCGCGC CTATAAATAC AGCCCGCAAC GATCTGGTAA ACACAGTTGA ACAGCATCTG

547 TTCGAATTTA AAGCTTGATA TCGAATTCCT GCAGCCCGAGC GCTGGATCCT CGATCACAAG
 AAGCTTAAAT TTCGAACTAT AGCTTAAGGA CGTCGGGTCG CGACCTAGGA GCTAGTGTTT

609
 607 TTT
 AAACATGTTT

2292
 ... Pro Ala Phe Leu Tyr Lys Val Val
 C TTG TAC AAA GTG GTG
 TTT CAC CAC

attB1

attB2

V5 epitope

2308 Ile Asp Pro Gly Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn
 ATC GAC CCG GGT CTA GAG GGC CCG CGG TTC GAA GGT AAG CCT ATC CCT AAC
 TAG CTG GGC CCA GAT CTC CCG GGC GCC AAG CTT CCA TTC GGA TAG GGA TTG

6xHis tag

2359 Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly His His His His His
 CCT CTC CTC GGT CTC GAT TCT ACG CGT ACC GGT CAT CAT CAC CAT CAC CAT
 GGA GAG GAG CCA GAG CTA AGA TGC GCA TGG CCA GTA GTA GTG GTA GTG GTA

OplE2 Reverse priming site

2410 ***
 TGA GTTTATCTGA CTAATATCTTA GTTTGTATTG TCATGTTTAA ATACAATATG
 ACT CAAATAGACT GATTAGAAAT CAAACATAAC AGTACAAAAT TATGTTATAC

FIG. 17

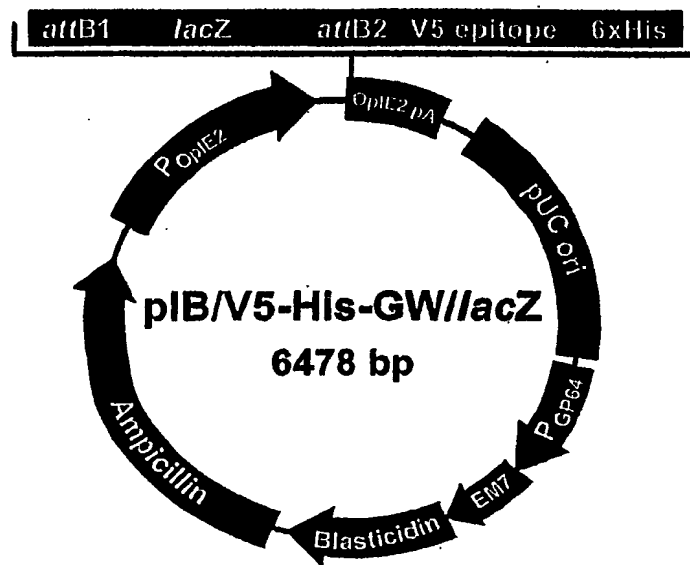


FIG. 18

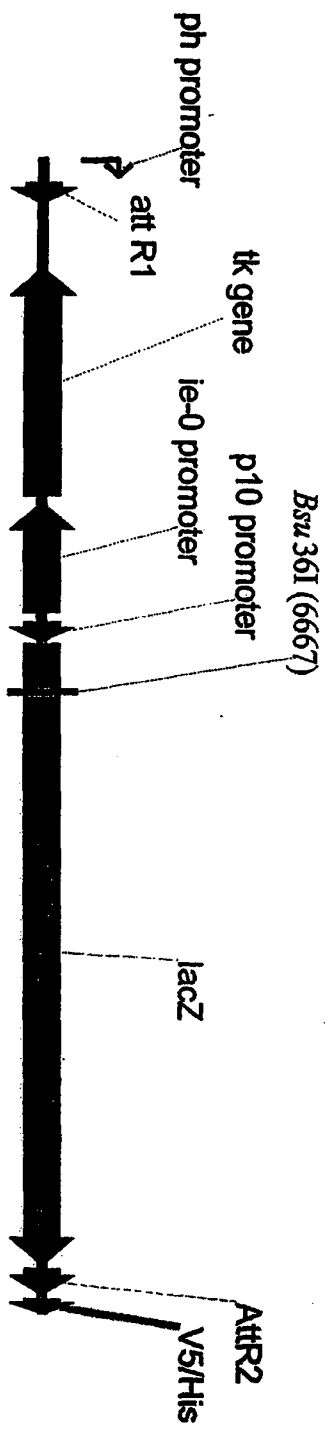


FIG. 19A

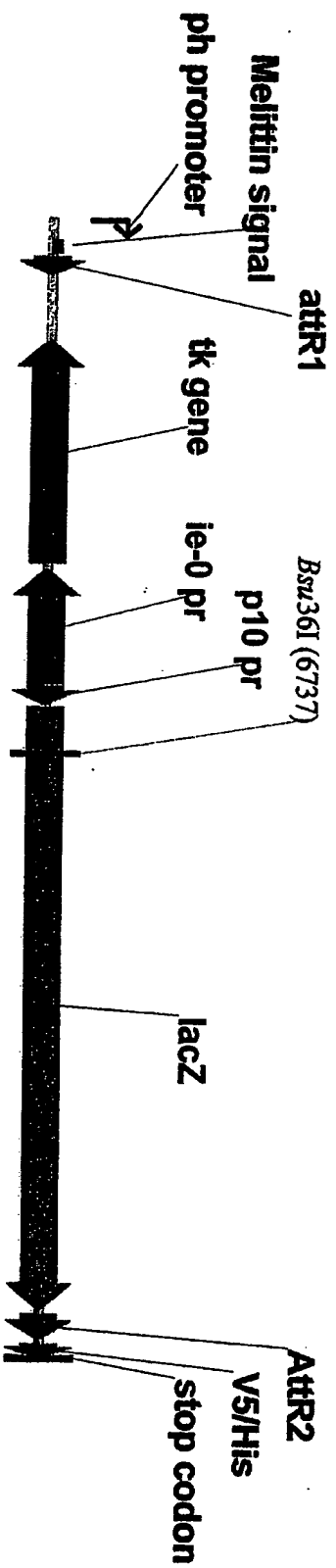


FIG. 19B

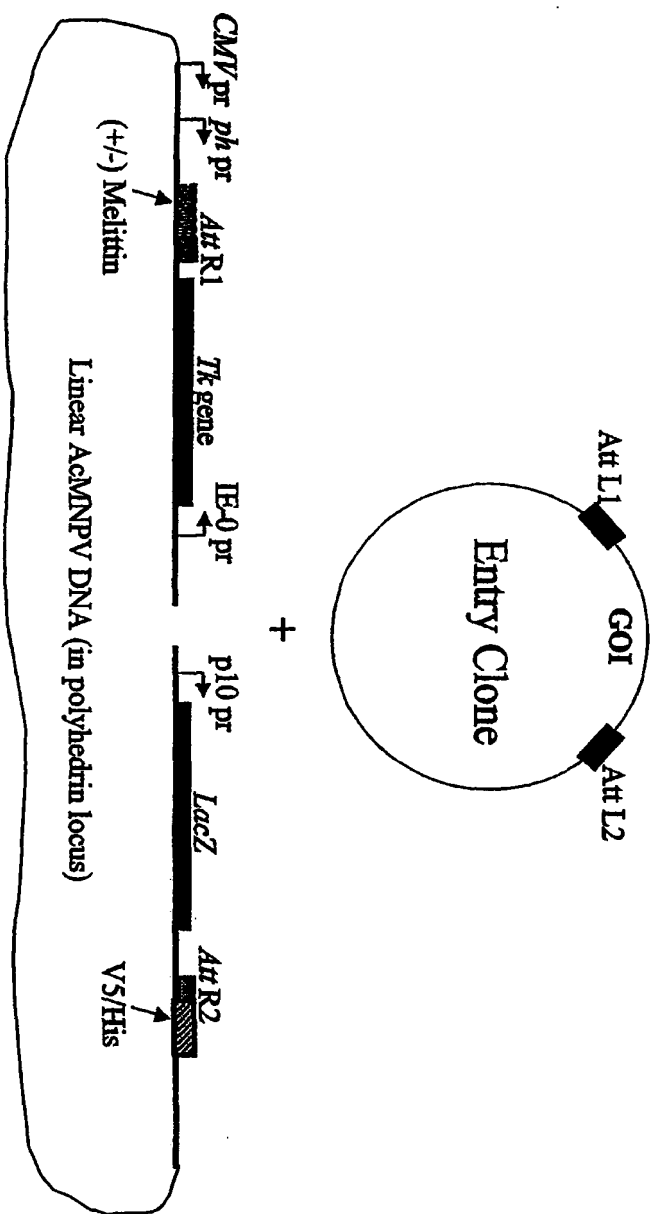
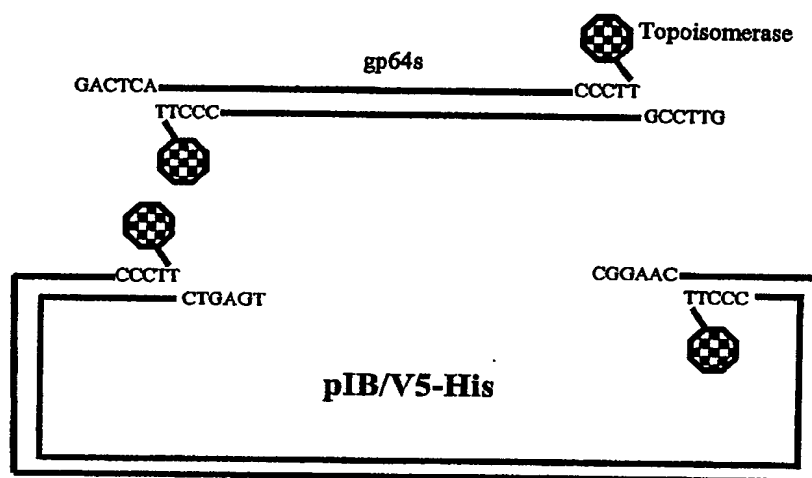


FIG. 20

FIG. 21



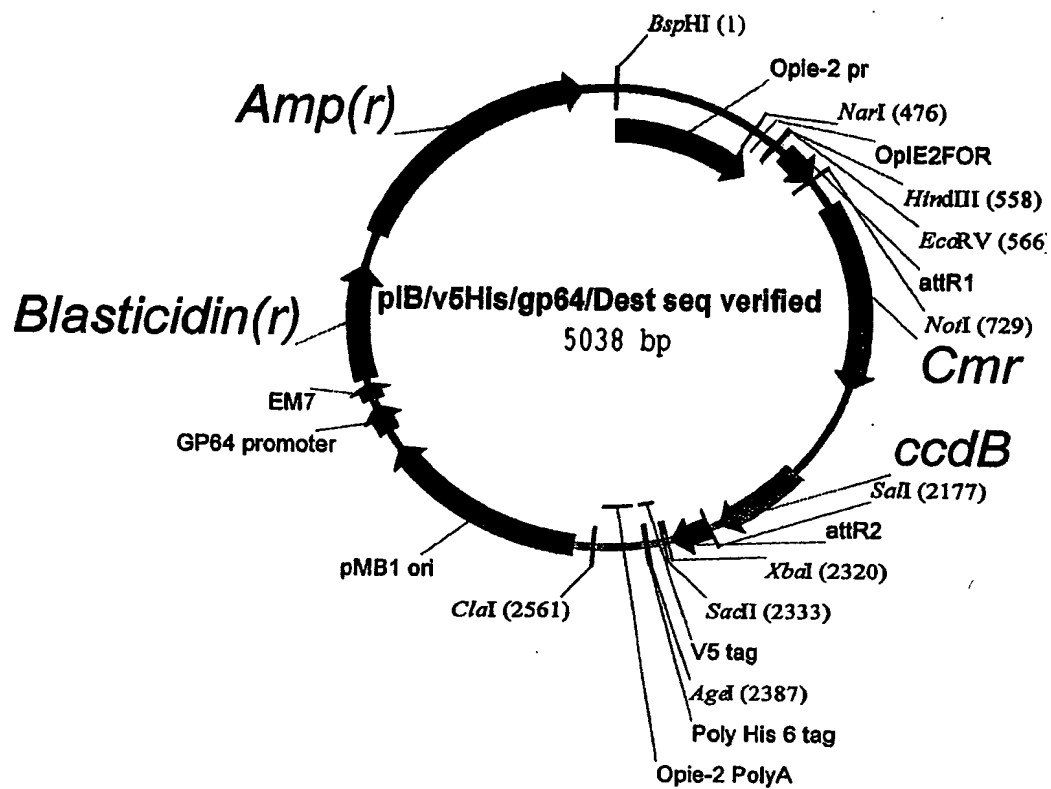


FIG. 22

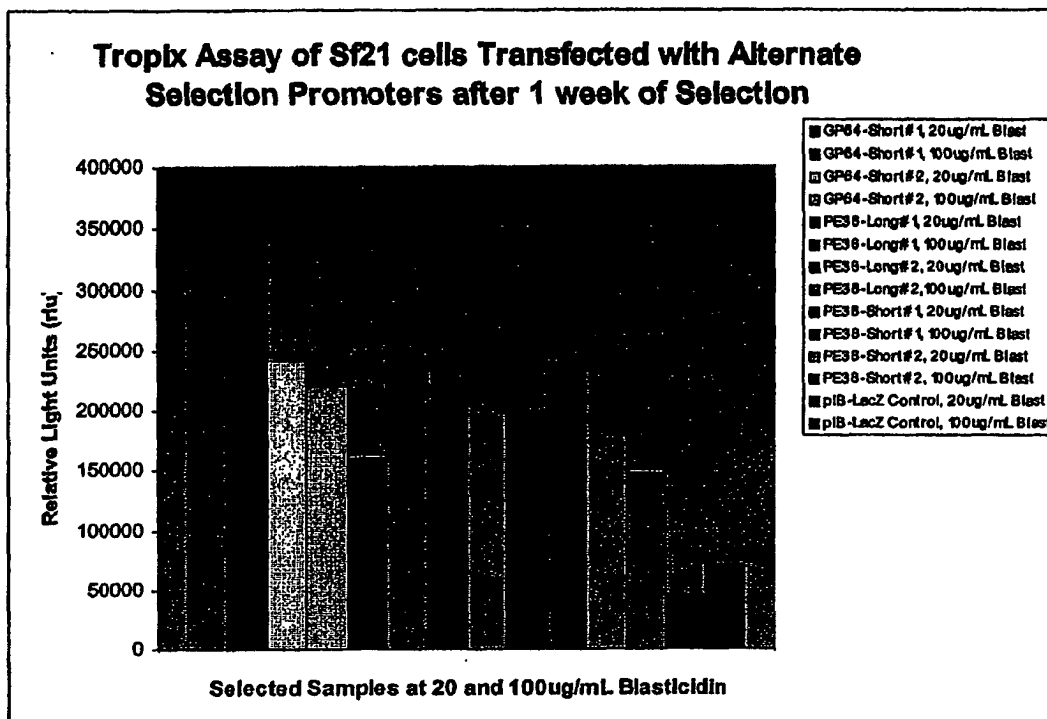


FIG. 23

FIG. 24

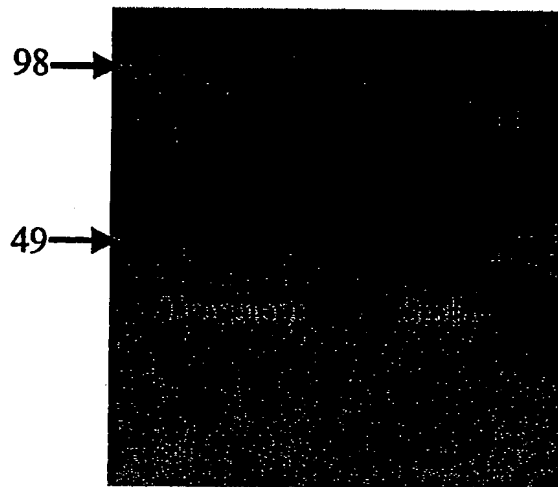
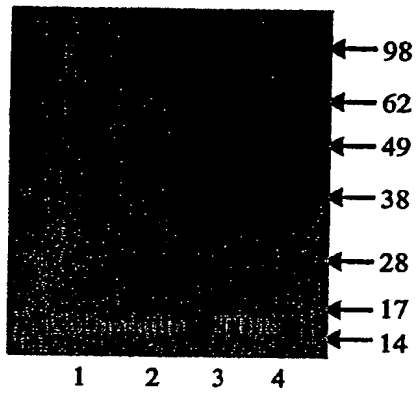


FIG. 25

A.



B.

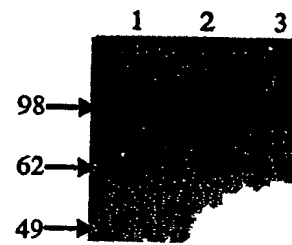
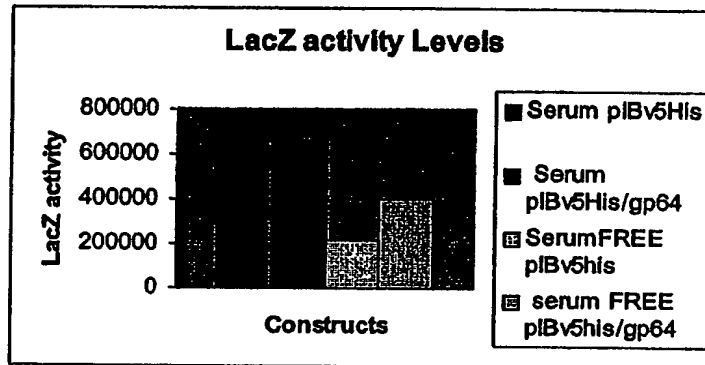


FIG. 26



Construction Phase: Purification

Destination Virus Stock (Reinforced)

Flanking region

attR1

ph promoter

HSV1 tk

le0

p10

Lac-Z

Acl

Flanking region

attR2

attR1

Early clone

Gene of interest

attL3

attR3

Transcription (Selectivity) Selection

Expression virus DNA (polymerized)

ph promoter

Gene of interest

attR2

attR1

Flanking region

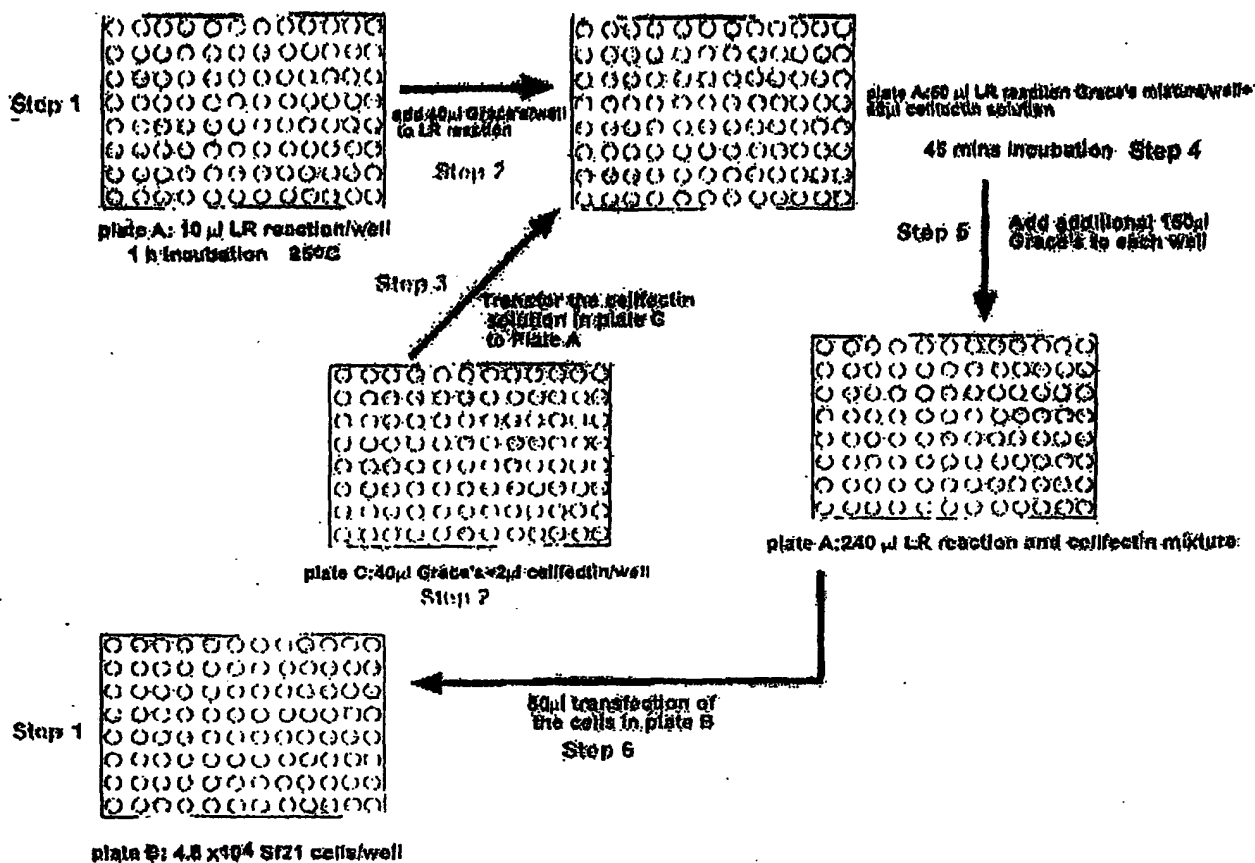


FIG. 28

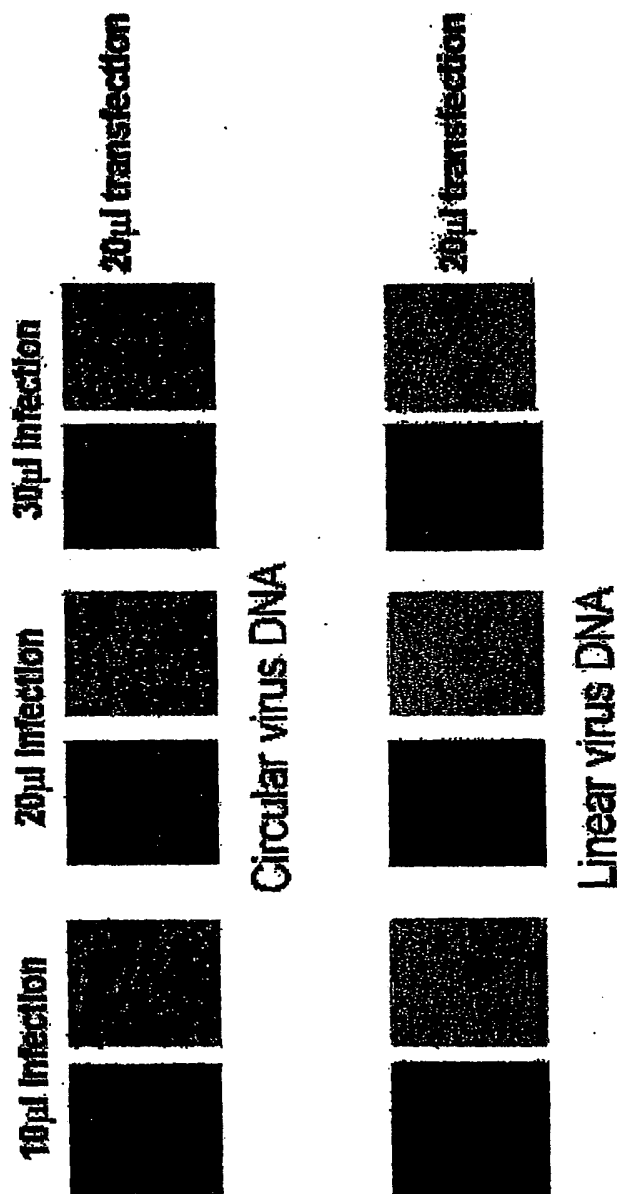


FIG. 29

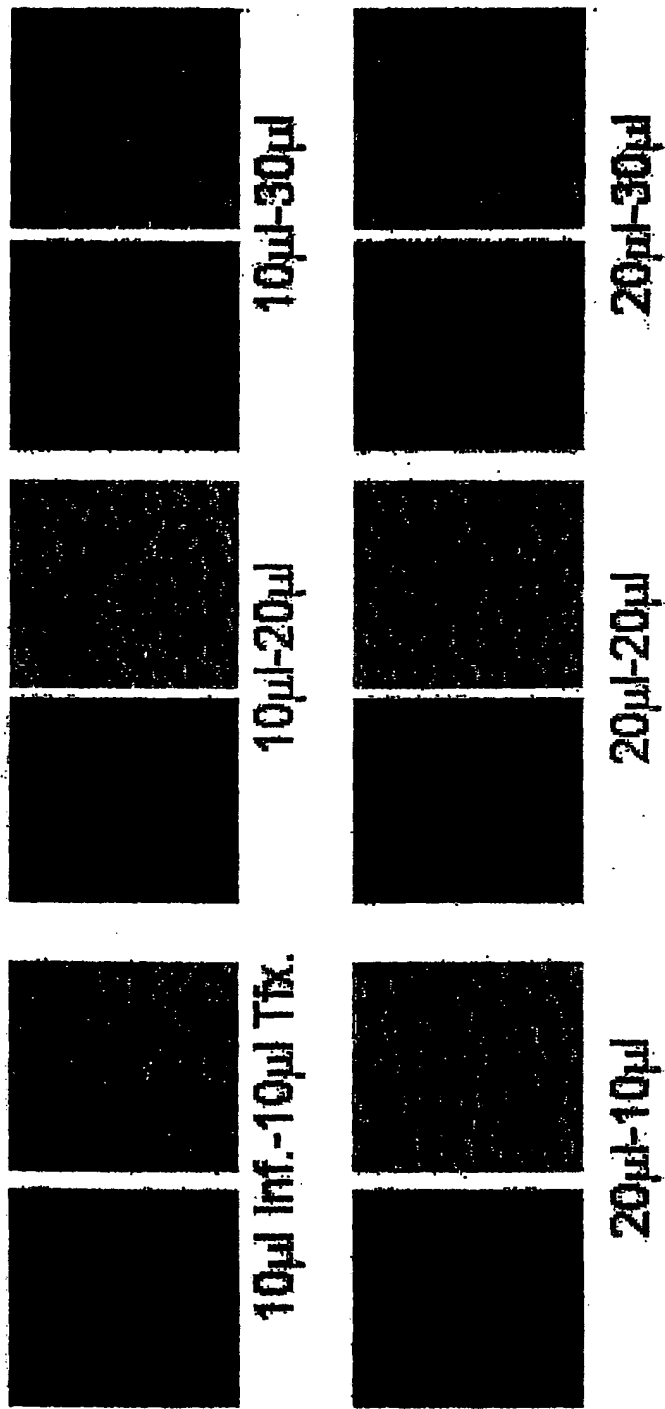


FIG. 30

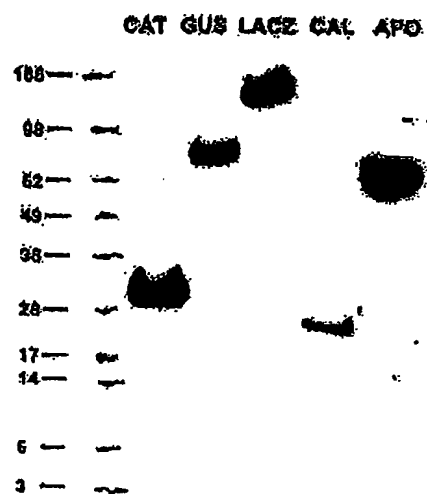


FIG. 31

Virus \ Titer pfu/ml	Transfect.	Infect.
Baculodirect™	9.8×10^6	6.9×10^8
Bac to Bac	6.9×10^6	7.2×10^8
MaxBac	N/A	3.6×10^8

Titer comparison of the three viruses by using TCID₅₀

Virus \ Titer pfu/ml	Transfect.	Infect.
Baculodirect™	6×10^6	3×10^8
Bac to Bac	8×10^6	5×10^8
MaxBac	N/A	3×10^8

Titer comparison of the three viruses by using plaque assay

FIG. 32

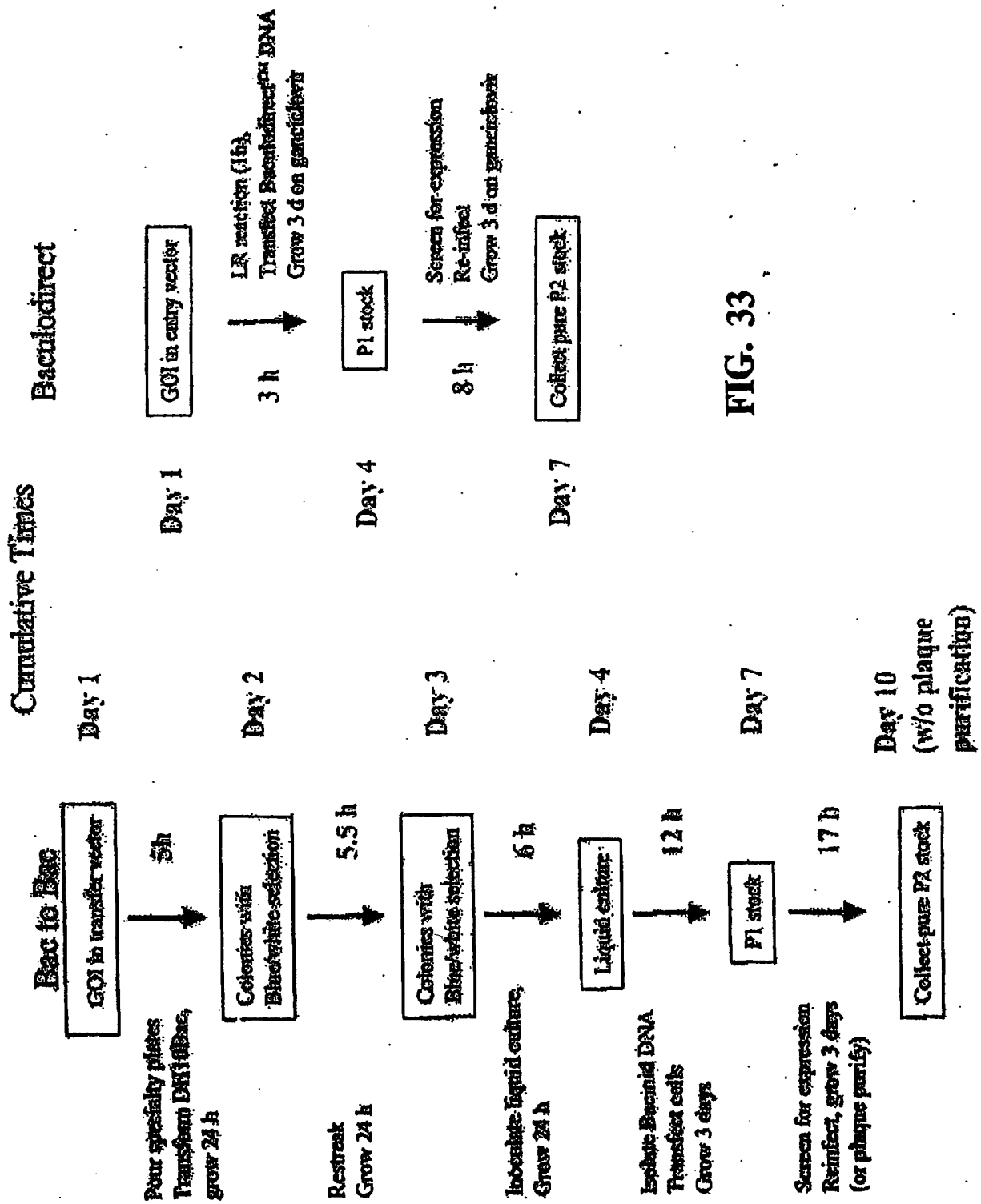


FIG. 33

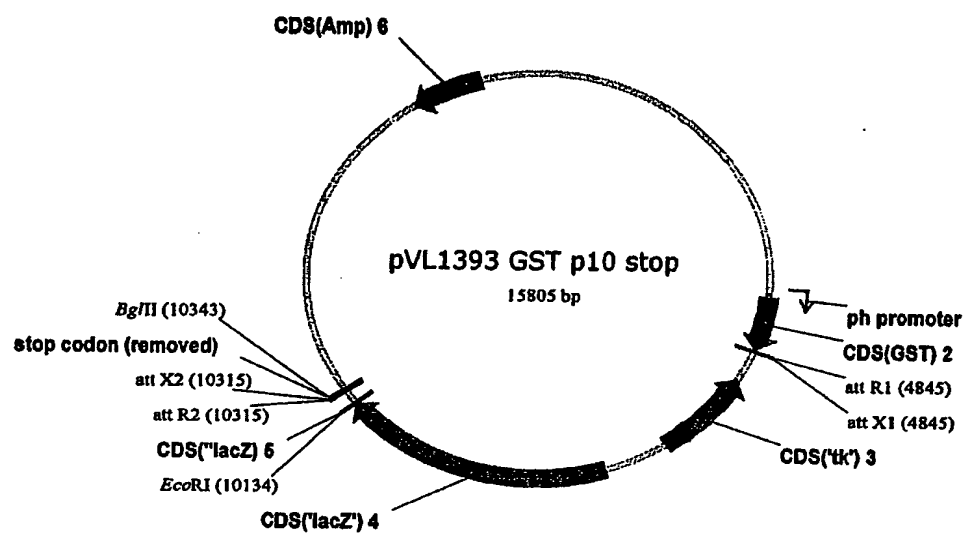


FIG. 34

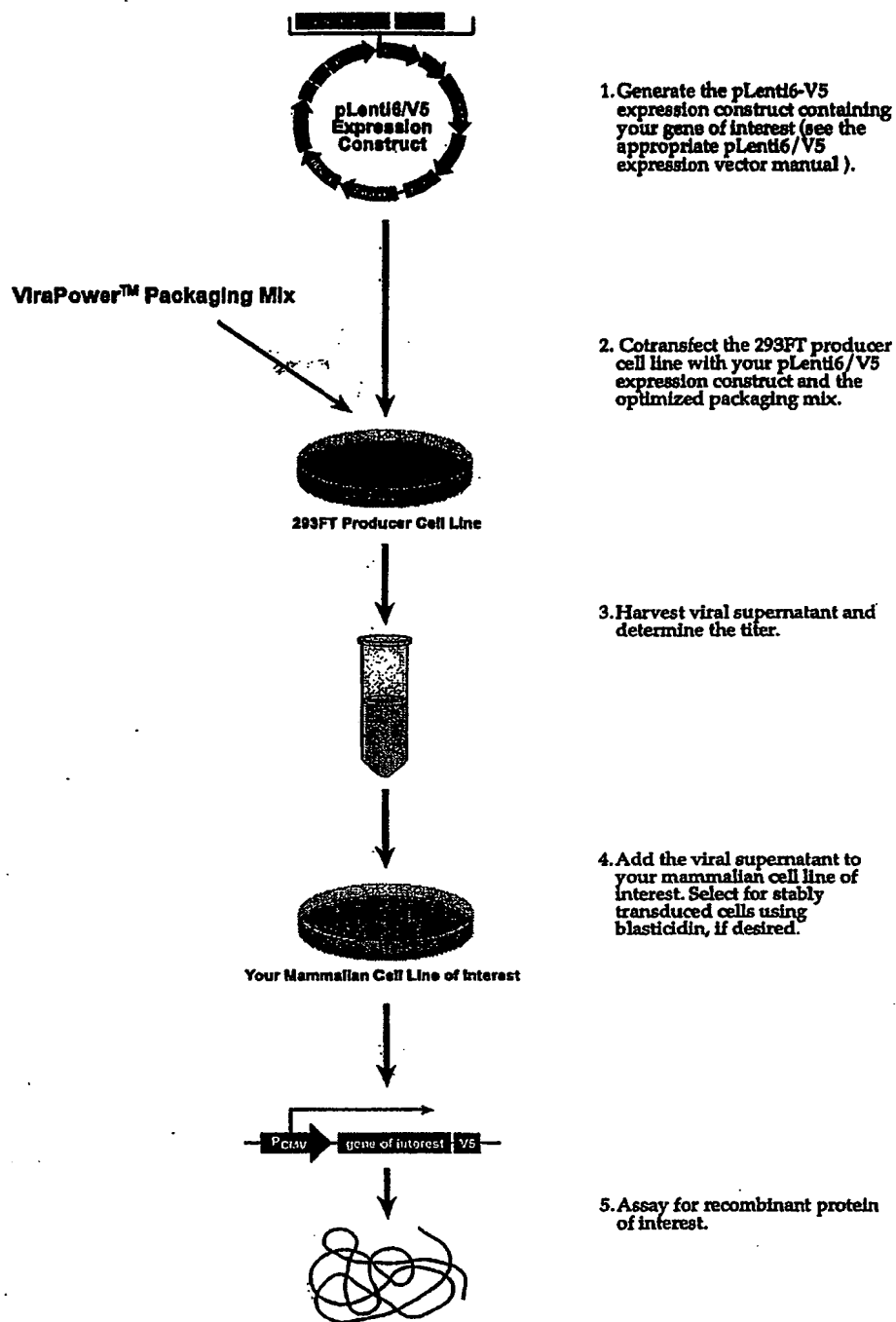
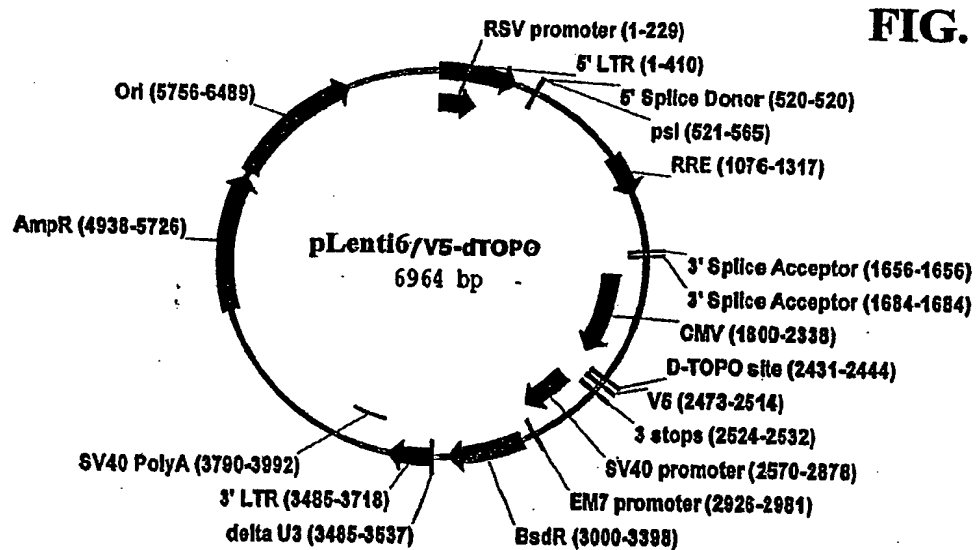
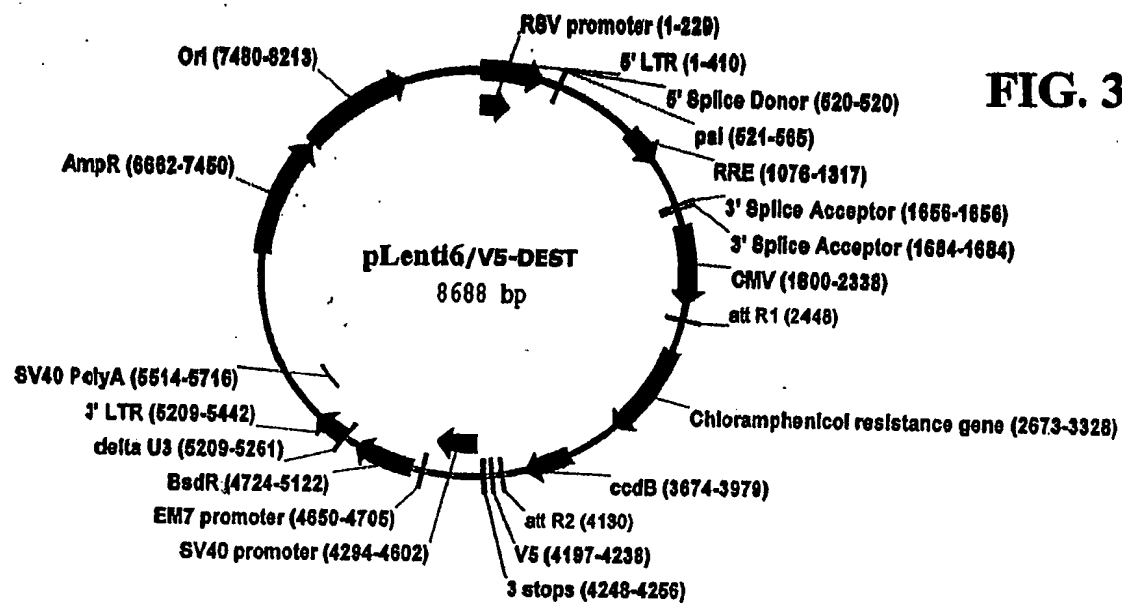


FIG. 35



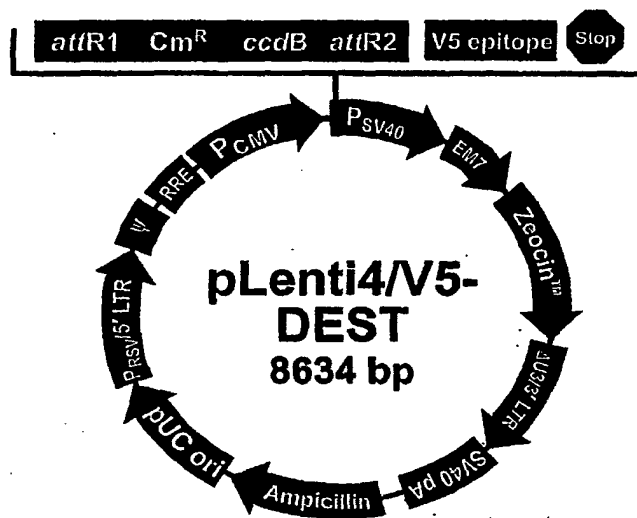


FIG. 36C

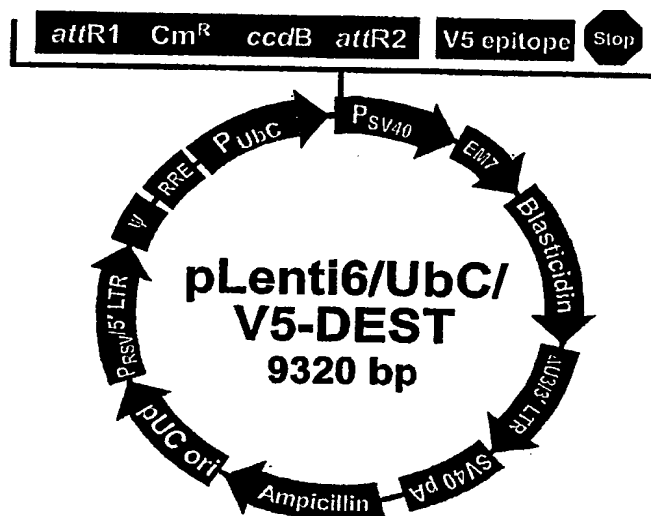


FIG. 36D

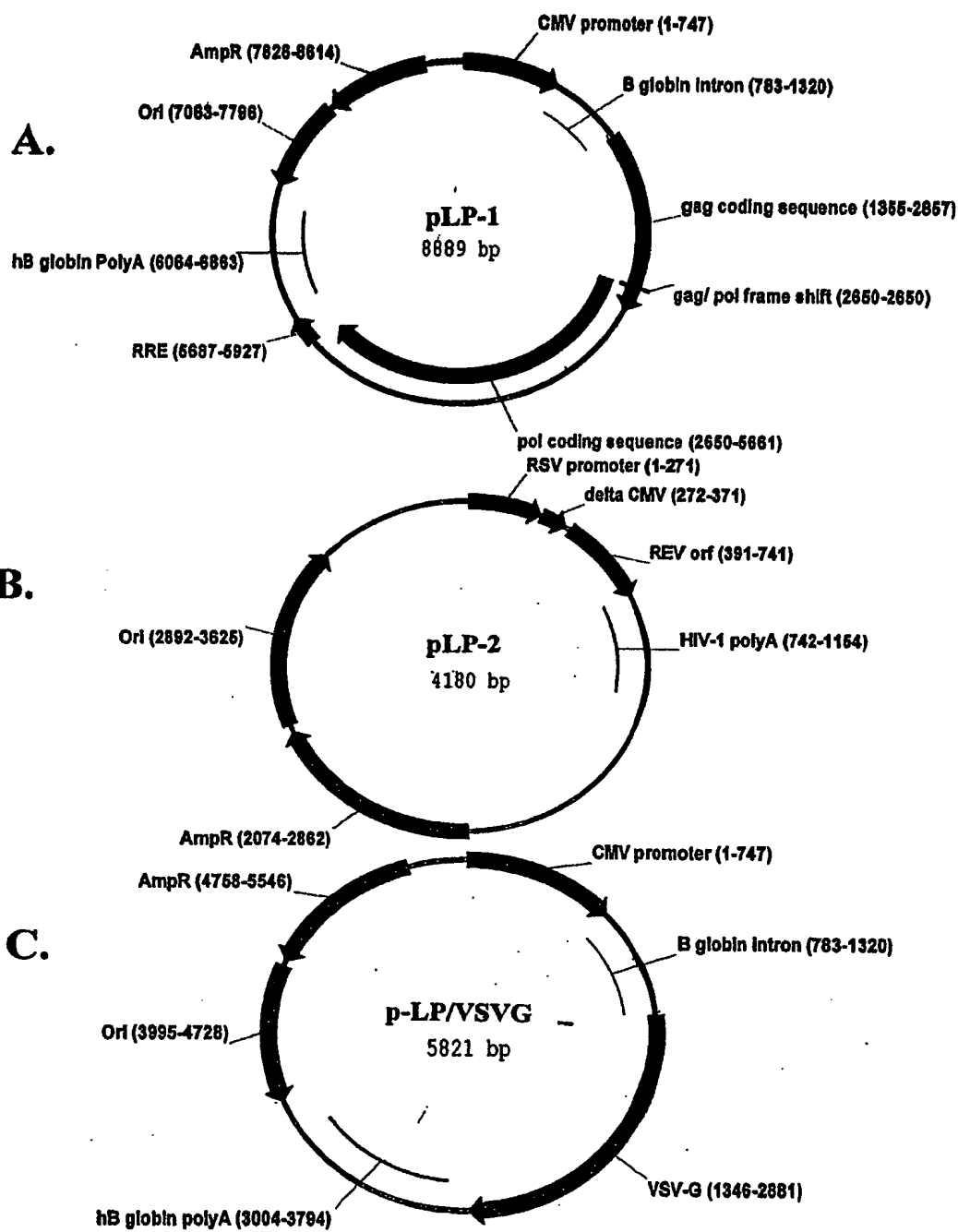
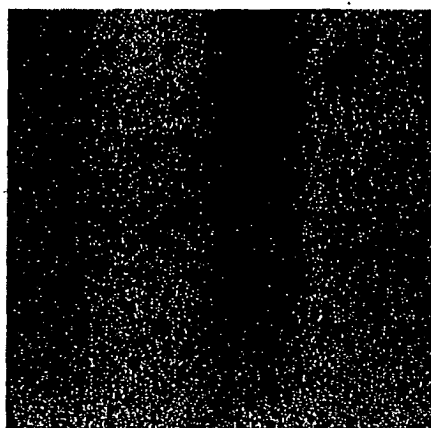


FIG. 37

A.



B.

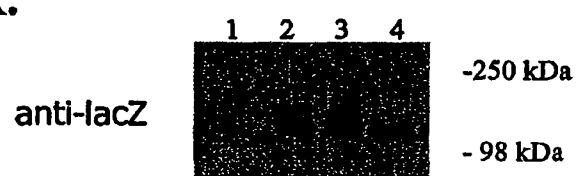
LR reaction [Bsd] in plate	DEST alone	DEST + CAT
No Bsd	24	320 ¹ (12/24 = 50%) ²
50 ug/ml Bsd	0	162 (24/24 = 100%) ²

¹see photo above

²percentage of correct colonies

FIG. 38

A.



B.

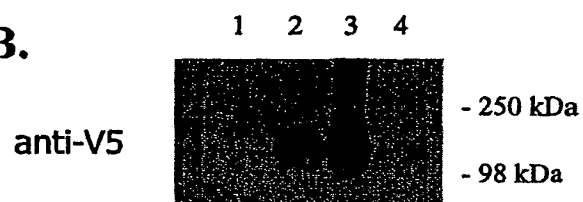


FIG. 39

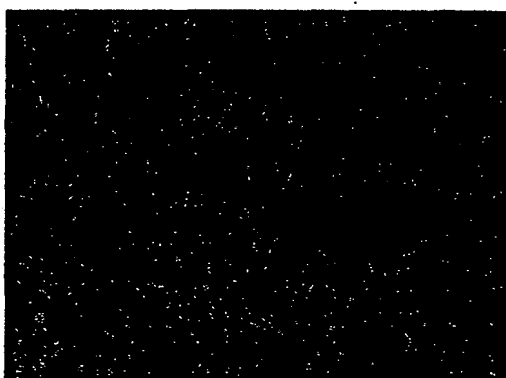
Examples of Production Titers (Bsd^R cfu/ml)

	Empty	LacZ	GFP	CAT	PKC
Exp 1	6×10^6	5×10^5	4×10^6	n.d.	n.d.
Exp 2	3×10^7	3×10^5	6×10^6	8×10^6	n.d.
Exp 3	7×10^6	6×10^5	2×10^6	1×10^7	3×10^6
AVG	1.4×10^7	4.7×10^5	4×10^6	9×10^6	3×10^6

n.d. = not determined

FIG. 40

A.



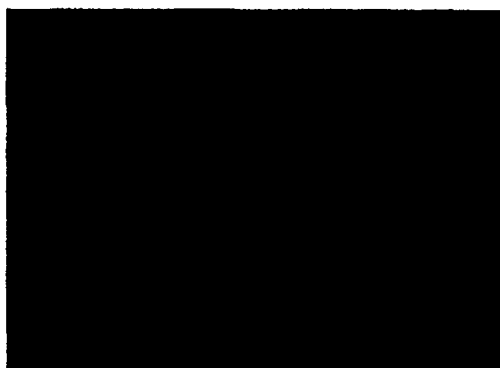
pLenti6/V5-GW/lacZ

B.



Brightfield

C.

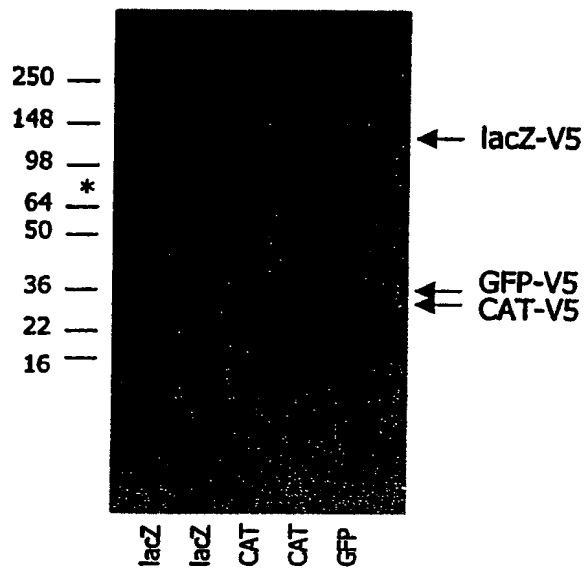


Fluorescent

pLenti6/V5-dT/GFP

FIG. 41

A.



B.

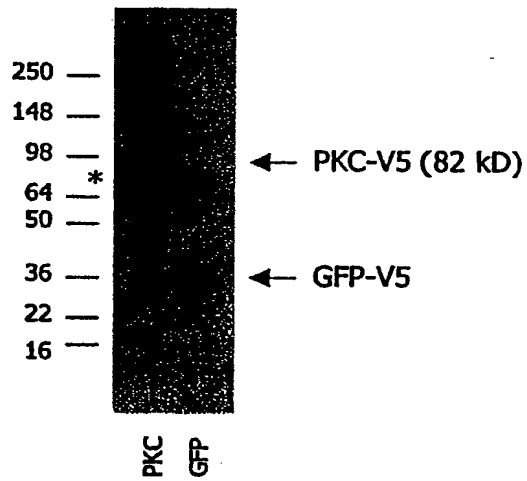
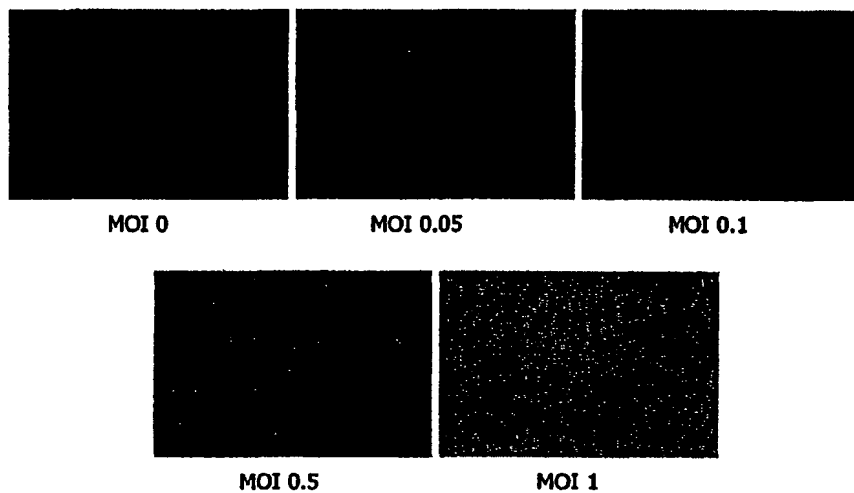


FIG. 42

A.



B.

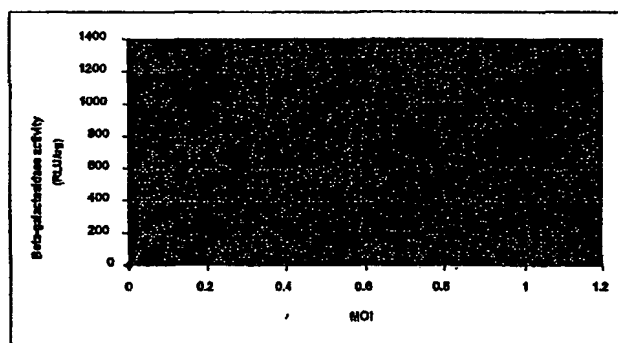
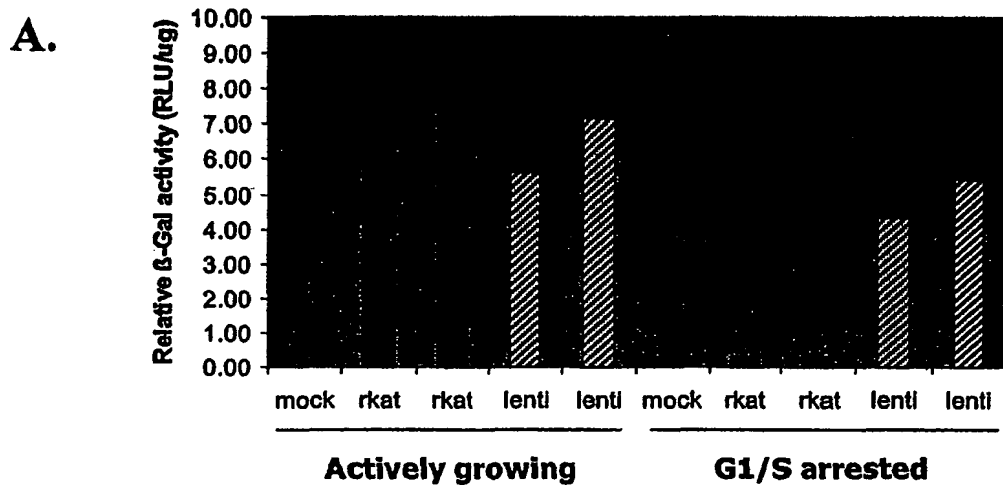
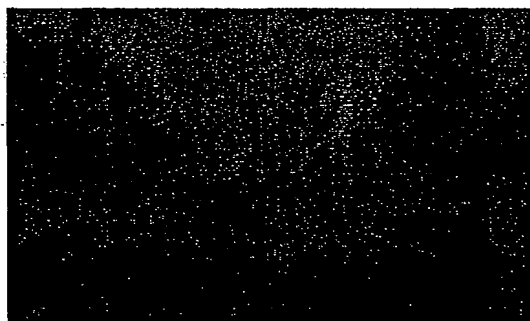


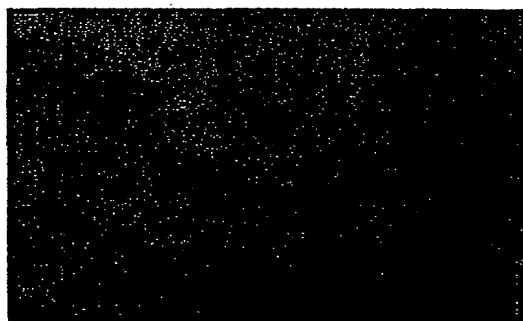
FIG. 43



B.



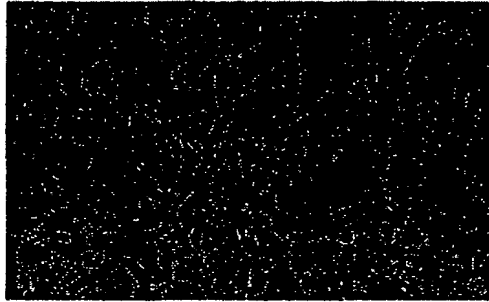
rKAT6-lacZ retrovirus



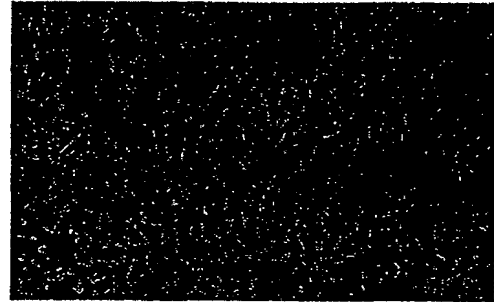
pLenti6/V5-GW/lacZ

FIG. 44

A.
10 days

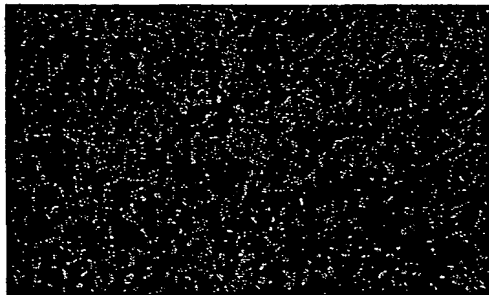


rKAT6-lacZ retrovirus

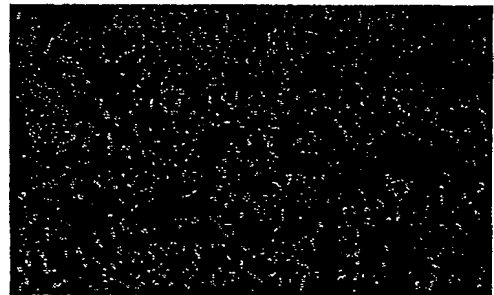


pLenti6/V5-GW/lacZ lentivirus

B.
6 weeks



rKAT6-lacZ retrovirus



pLenti6/V5-GW/lacZ lentivirus

FIG. 45

FIG. 46A

2251 TCGTAACAAC TCCGCCCAT TGACGCAAT GGC CGGTAGG CGTGACGGT GGGAGGTCTA TATAAGCAGA GCTCGTTTAG

2331 TGAACCGTCA GATCGCCTGG AGACGCCATC CACGCTGTTT TGACCTCCAT AGAAGACACC GACTCTAGAG GATCCACTAG

2411 TCCAGTGTGG TGGAATTCTG CAGATATCAA CAAGTTT ... Pro Ala Phe Leu

4134 TAC AAA GTG GTT GAT ATC CAG CAC AGT GGC GGC CGC TCG AGT CTA GAG GGC CCG CGG TTC GAA GGT

4200 TTC GGA TAG GGA TTC GGA GAG GAG CCA GAG CTA AGA TGC GCA TGG CCA ATC ATT ACT

Transcriptional start

CAAT CMV forward priming site TATA

2448 4130

attB1 attB2

V5 epitope V5 (C-term) reverse priming site

FIG. 46B

US forward priming site

2881 TTGGCGAGTG TGTTTTGTGA AGTTTTTTAG GCACCTTTTG AAATGTAATC ATTTGGGTCA ATATGTAATT TTCAGTGTTA

2961 GACTAGTAAA TTGTCCGCTA AATTCTGGCC GTTTTGGGCT TTTTGTGTAG ACGAAGCTTG GTACCGAGCT CGGATCCACT

3041 AGTCCAGTGT GGTGGAATTC TGCAGATATC AACAAAGTTT ... Pro Ala Phe
ACGTCATAG TTGTTCAAAC ATGTTT

3078 4762

atB1 atB2

4763 Leu Tyr Lys Val Val Asp Ile Gln His Ser Gly Gly Arg Ser Ser Leu Glu Gly Pro Arg Phe Glu
TTG TAC AAA GTG GTT GAT ATC CAG CAC AGT GGC GGC CGC TCG AGT CTA GAG GGC CCG CGG TTC TTA GAA
TTT CAC CAA CTA TAG GTC GTG TCA CCG CCG GCG AGC TCA GAT CTC CCG GGC GCC AAG CTT

4829 Gly Lys Pro Ile Pro Asn Pro Leu Leu Cys Ser Thr Arg Thr Gly *** *** ***
GGT AAG CCT ATC CCA AAC CCT CTC CTC GGT CTA GAT TCT ACG CGT ACC GGT TAG TAA TGA GTTT
CCA TTC GGA TAG GGA TTC GGA GAG GAG CCA GAG CTA AGA TGC GCA TGG CCA

V5 epitope V5 (C-term) reverse priming site

FIG. 46C

1786 ^{5' end of UbO promoter}
 CGGATCTGGC CTCCGCGCGG GGTTTTGCGC CTTCCGCGCG GCGCCGCCCT CCTCACGGCG AGCGCTGCCA CGTCAGACGA
 1876 ^{Sp 1}
 AGGGCGCAGG AGCGTCTGA TCCTTCCGCC GCGACGCTCA GGACAGCGGC CCGCTGCTCA TAAGACTCGG CCTTAGAACC
 1956 CCACTATCAG CAGAAGGACA TTITAGGACG GGACTTGGGT GACTCTAGGG CACTGGTTTT CTTCCAGAG AGCGGAACAG
 2036 GCGAGGAAAA GTAGTCCCTT CTCCGCGATT CTGCGGAGGG ATCTCCGTG ^{Sp 1} ^{TATA box}
 GCGCGTGAAC GCGATGATT ATATAAGGAC
 2116 ^{Start of Transcription}
 GCGCCGCGTG TGCCACAGCT AGTTCGCTCG CAGCCGGGAT TTGGGTCGCG GTTCTTGTTT GTGGAICGCT GTGATCGTCA
 Exon 1
 2196 ^{5' end of Intron 1}
 CTTGTGAGT AGCGGGCTGC TGGGCTGGCC GGGGCTTTCG TGGCGCCCGG GCGCTCGGT GGGACGGAAG CGTGTGGAGA
 2276 GACGCCAAGG GGCTGTAGTC TGGGTCGCG AGCAAGGTTG CCTGAACTG GGGGTGGGG GGAGCGCAGC AAAATGGCGG
 2356 CTGTTCCCGA GTCTGAATG GAAGACGCTT GTGAGGCGGG CTGTGAGTC GTTGAACAA GGTGGGGGGC ATGTTGGGGC
 2436 GCAAGAACCC AAGGTCTTGA GGCCTTCGCT AATGCGGAA AGCTCTTATT CCGGTGAGAT GGGCTGGGGC ACCATCTGGG
 2516 GACCCGACG TGAAGTTGT CACTGACTGG AGAACTCGGT TTGTCGTCTG TTGCGGGGCG GGCAGTTATG CGGTGCCGTT
 2596 GGGCAGTCCA CCGTACCTT TGGGAGCGCG CCGCCTCGTC GTGTCGTGAC GTACCCGTT CTGTTGGCTT ATAATGCAGG
 2676 GTGGGGCCAC CTGCCGCTAG GTGTGCGGTA GGTCTTTCTC CGTCGCAGGA CGCAGGGTTC GGGCTAGGG TAGGCTCTCC
 2756 TGAATCGACA GCGCGCGGAC CTCGCTGAG GGGAGGGATA AGTGAGGCGT CAGTTTCTTT GGTGGTTTT ATGTACCTAT
 2836 CTTCTAAGT AGCTGAAGCT CCGGTTTGA ACTATGCGCT CGGGGTGGC GAGTGTGTTT TGTGAAGTTT TTTAGGCACC
 2916 ^{UB Forward priming site}
 TTTTGAATG TAATCATTTG GGTCAATAG TAATTTTCAG TGTAGACTA GTAAATGTC CGCTAAATTC TGGCCGTTTT
 2996 ^{5' end of Intron 1}
 TGGCTTTTTT GTTAGACGAA GCTTGG....
 5' end of Exon 2

FIG. 47

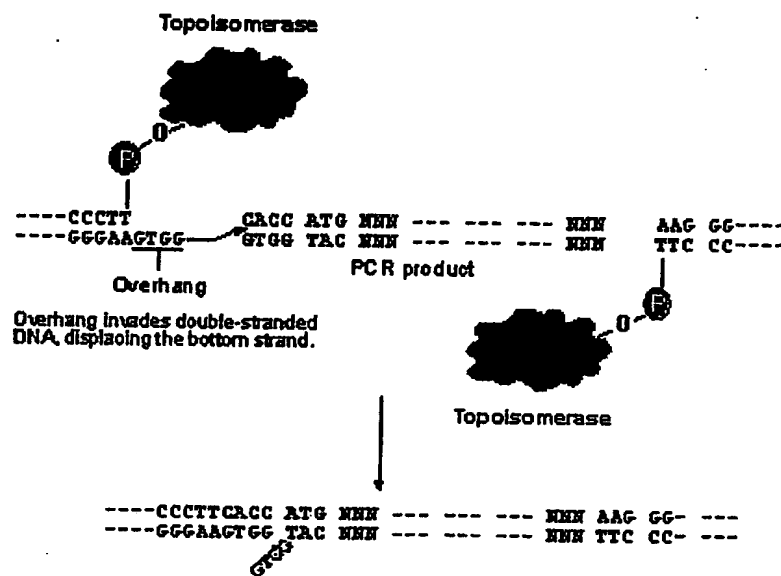
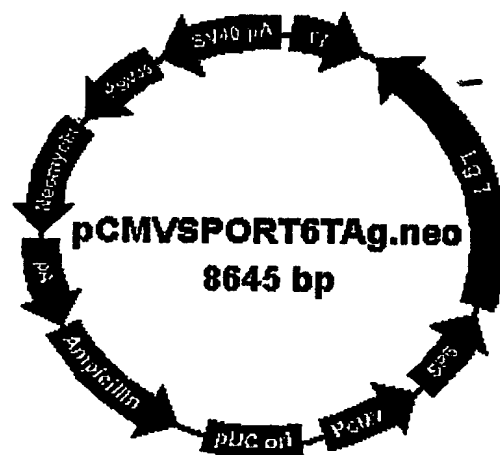


FIG. 48

2251 TCGTAACAAC TCCGCCCAT TGACGCAAAAT GGGCGGTAGG CGTGACGGT GGGAGGTCTA TATAAGCAGA GCTCGTTTAG
 CAAT CMV forward priming site TATA 3' end of CMV promoter
 2331 TGAACCGTCA GATCGCCTGG AGACGCCATC CACGCTGTTT TGACCTCCAT AGAAGACACC GACTCTAGAG GATCCACTAG
 Transcriptional start BamHI SpeI
 2411 TCCAGTGTGG TGGAATTGAT CCCTT ACC ATG ... AAG GGC TCG AGT CTA GAG GGC CCG CGG TTC GAA GGT
 BstXI XhoI ApeI SacII SstI
 CTA GGAAG TGC TAC ... TTC CCA GTT CTG
 Lys Gly Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly
 V5 epitope V5(C-term) reverse priming site
 2476 AAG CCT ATC CCT AAC CCT CTC CTC GGT CTC GAT TCT ACG CGT ACC GGT TAG TAA TGA GTTGGAA
 Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly *** *** ***
 2541 TTAATTCTGT

FIG. 49



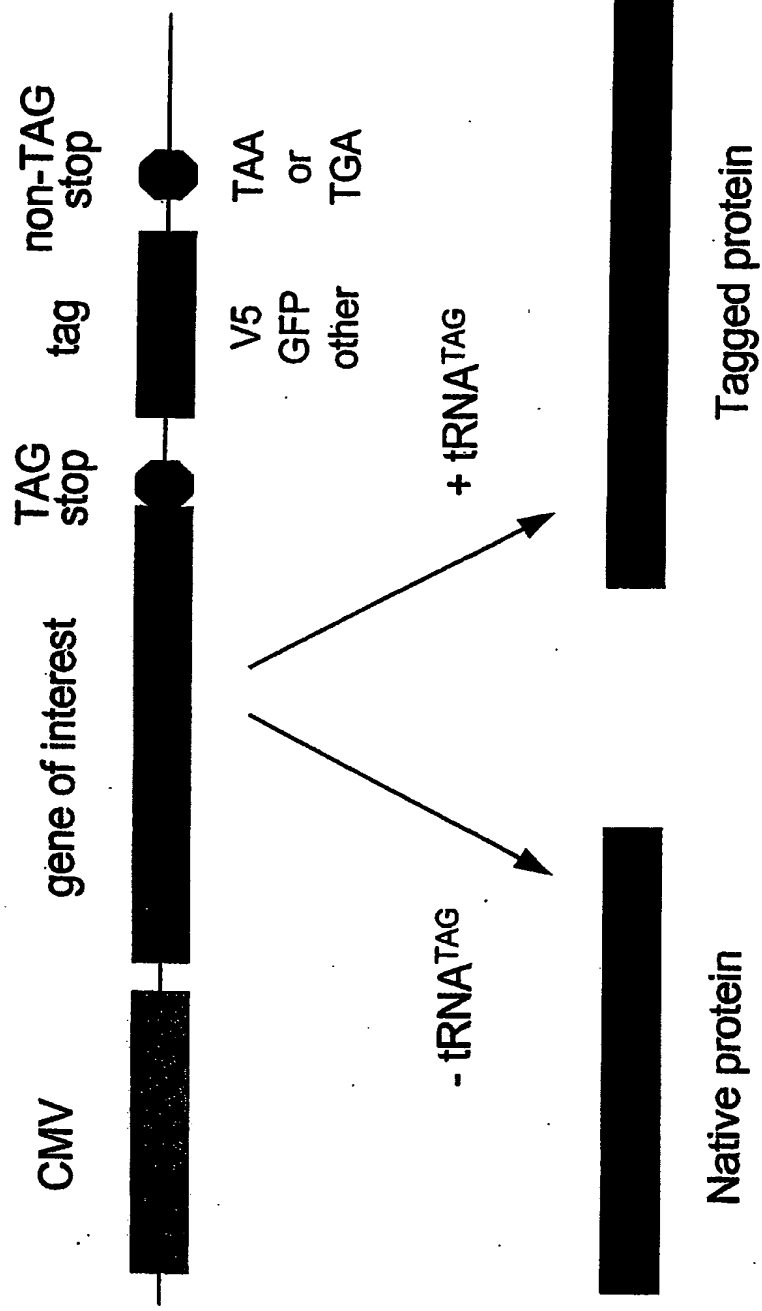


FIG. 50

FIG. 51A

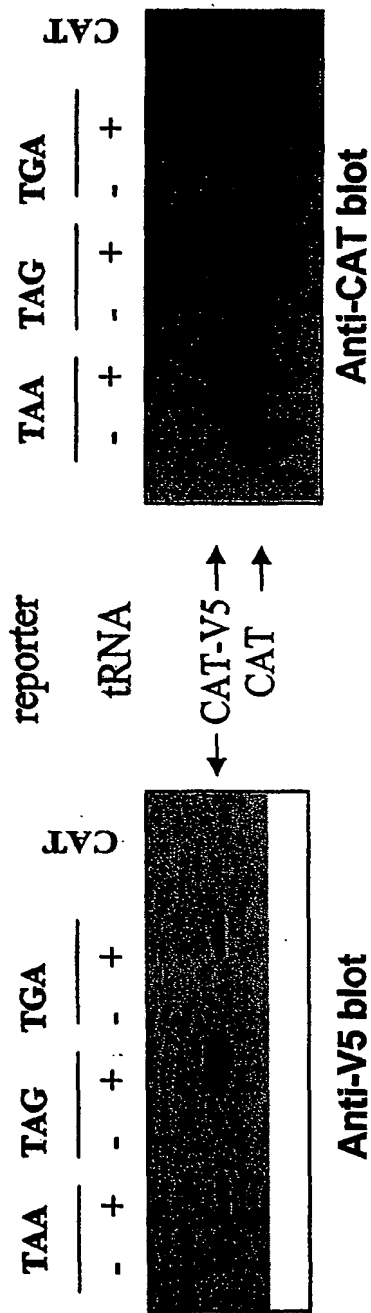
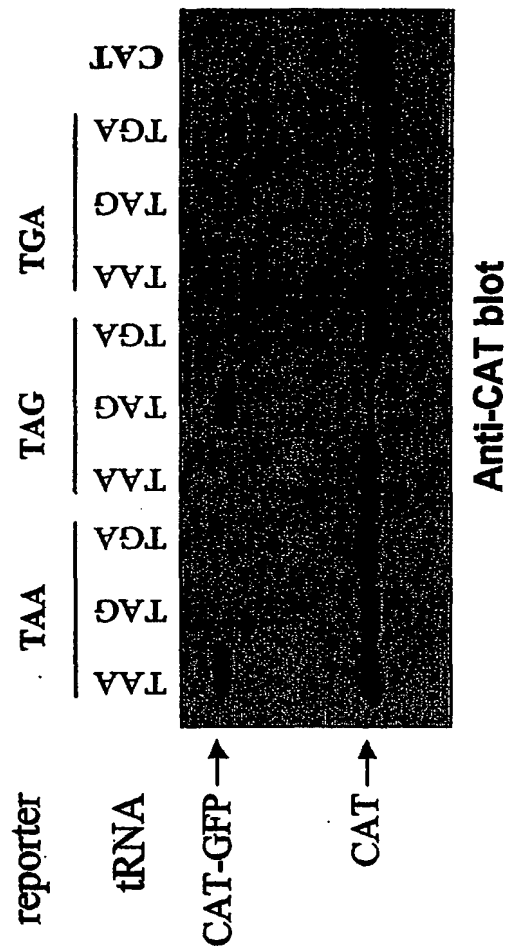


FIG. 51B



FIGS. 51 A-B

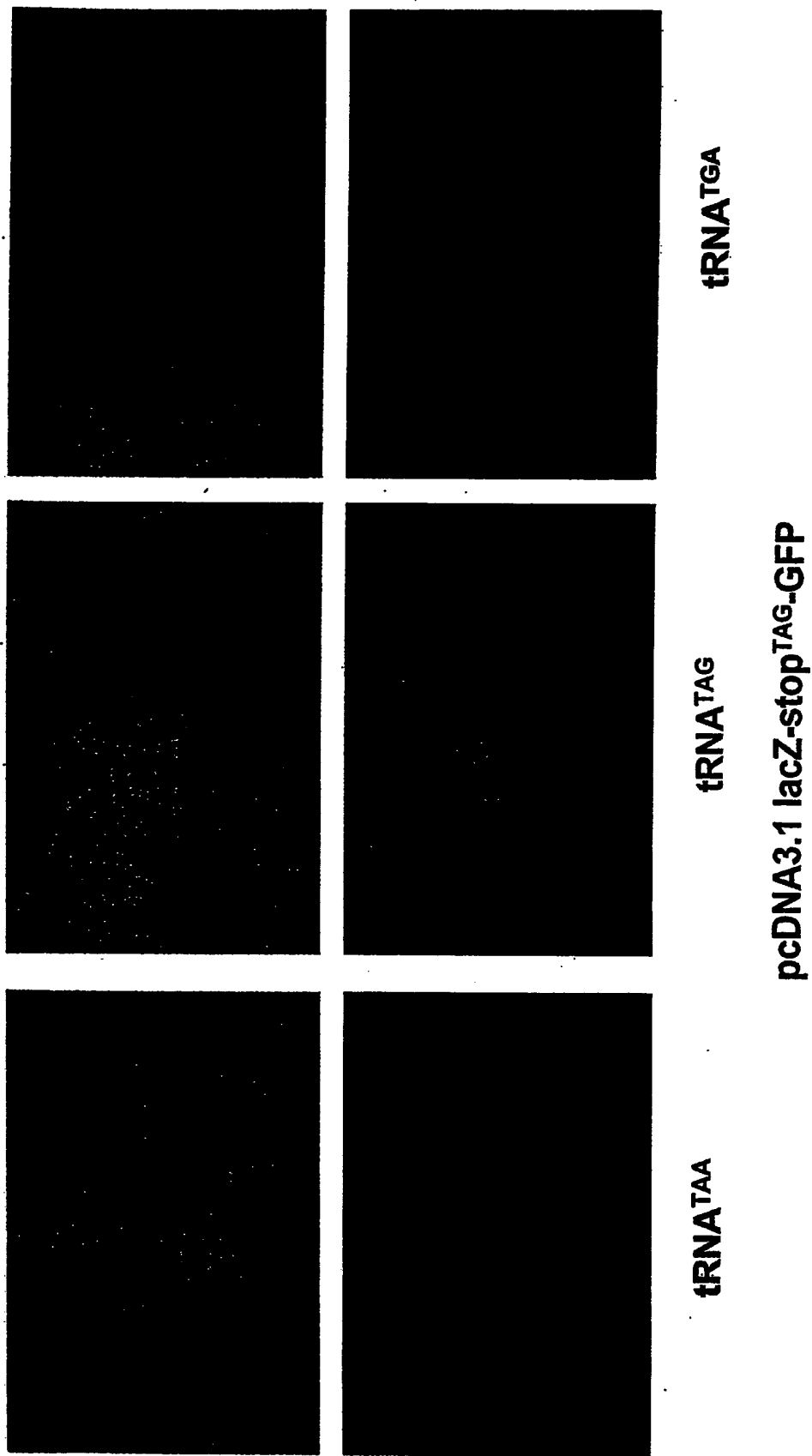


FIG. 52

Monomer

8-mer

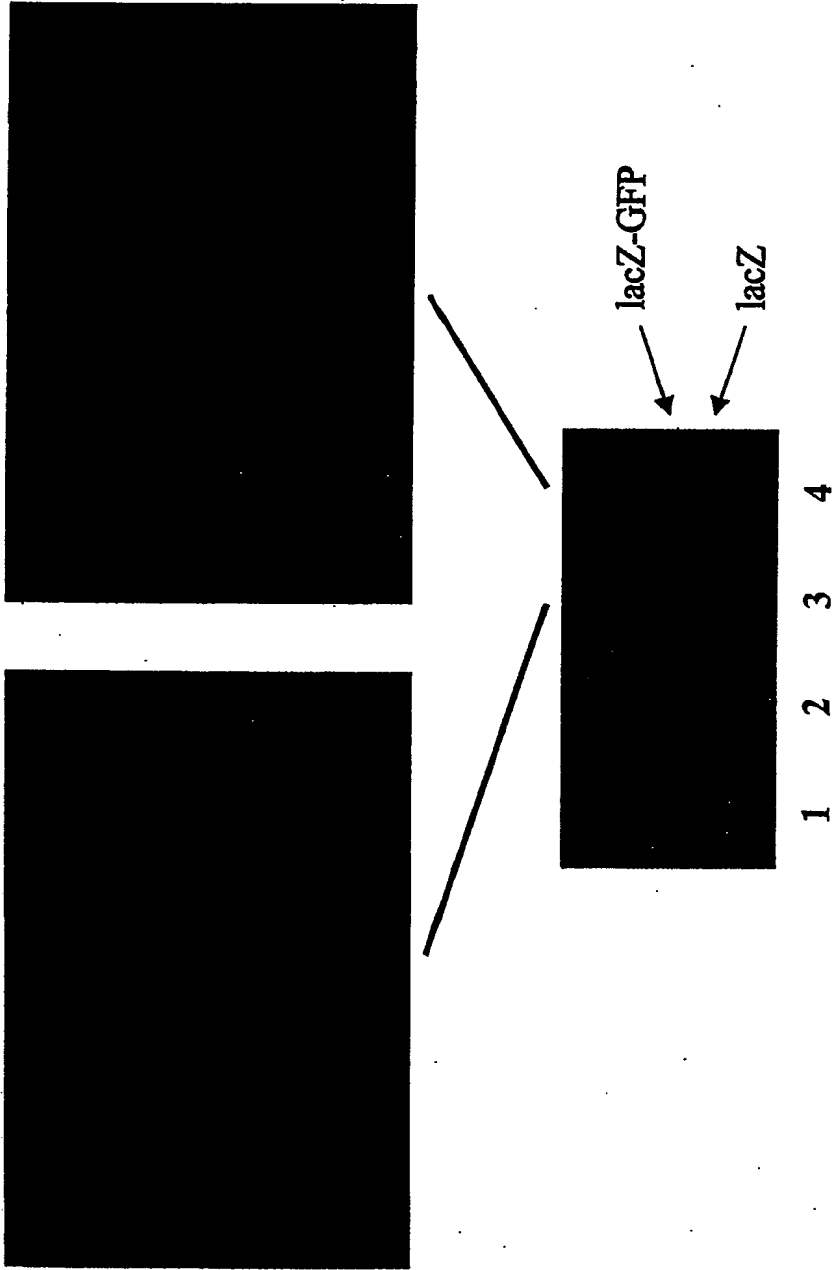
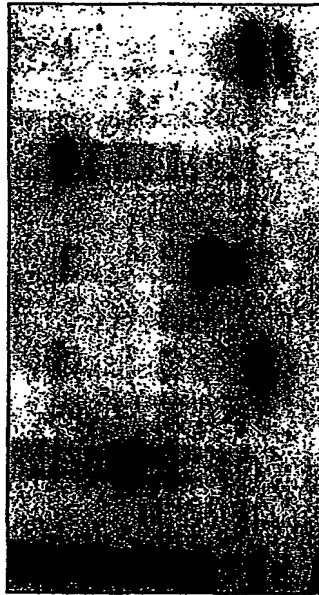


FIG. 53

[illegible][illegible]

	12	6	7	lacZ	
mock	-	+	-	+	+
GFP-V	-	+	+	-	-

mock
GFP-V5

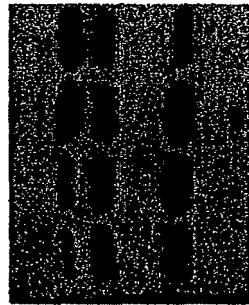


Anti-V5 blot

FIG. 54

FIG. 55A

MOI: 19 51 77 192



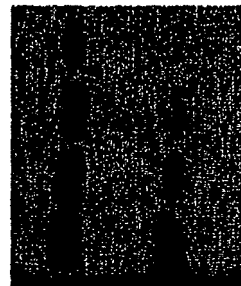
*

% suppression: 13 30 51 60

STABLE GOI

FIG. 55B

MOI: 19 38 77 192



% suppression: 63 71 76 75

TRANSIENT GOI






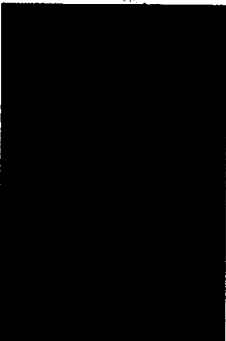




BHK-21	CHO-S	COS-7	HeLa	HT1080
				
				

FIG. 56

FIG. 57

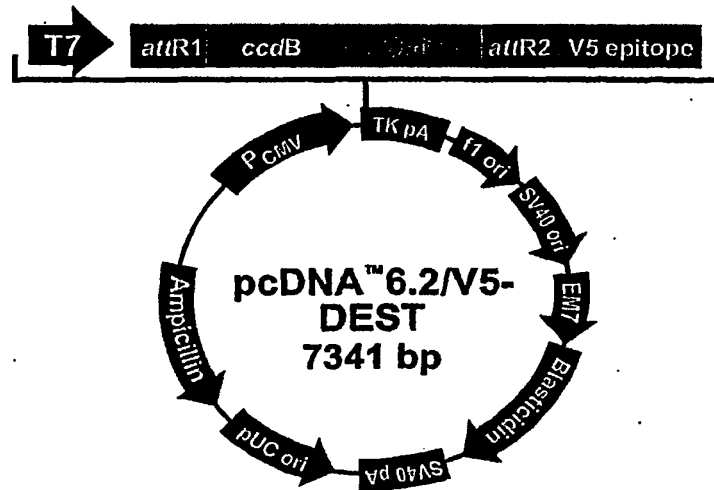


FIG. 58

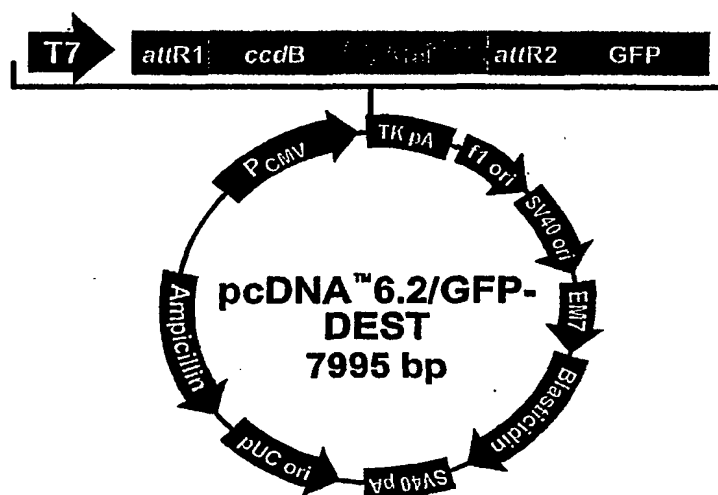


FIG. 59

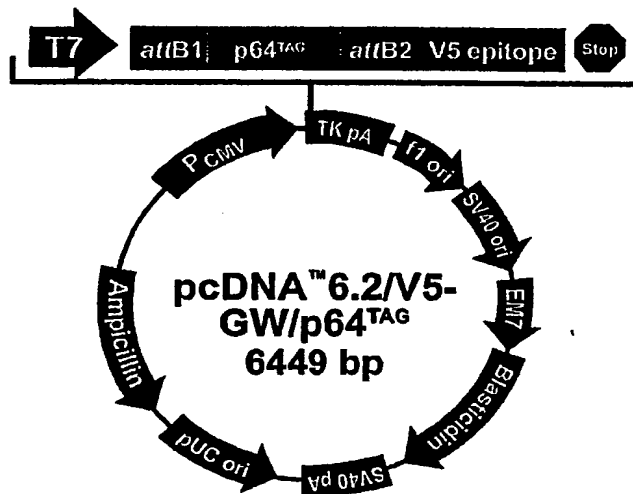


FIG. 60

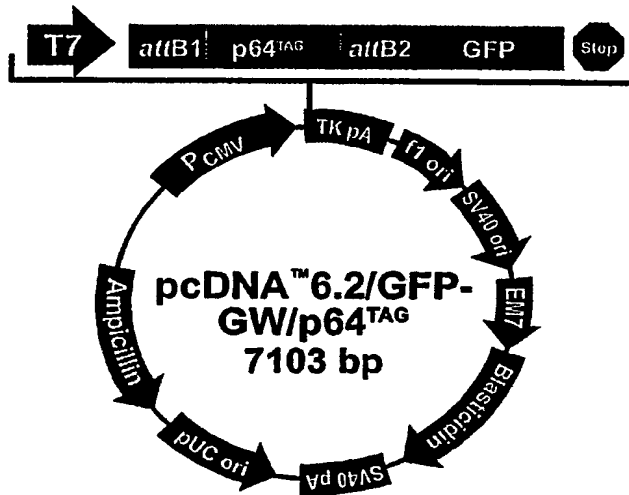


FIG. 61

A.

CAAT TATA 3' end of CMV promoter Putative transcriptional start
 771 CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA
 T7 promoter/priming site
 841 CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGT TAAGCTATCA
 918 attB 1 3161 attB 2
 911 ACAAGTTT TTT CAC CAA
 TGTTCAAACA TGTTT Pro Ala Phe Leu Tyr Lys Val Val
 V5 epitope V5 reverse priming site
 3177 GAT CTA GAG GGC CCG CGG TTC GAA GGT AAG CCT ATC CCT AAC CCT CTC CTC GGT CTC
 Asp Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu
 3234 GAT TCT ACG CGT ACC GGT TAG TAA TGA GTTTAAACGG GGGAGGCTAA CTGAAACACG
 Asp Ser Thr Arg Thr Glv *** *** ***

B.

CAAT TATA 3' end of CMV promoter Putative transcriptional start
 771 CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA
 T7 promoter/priming site
 841 CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGT TAAGCTATCA
 918 attB 1 3161 attB 2
 911 ACAAGTTT TTT CAC CAA
 TGTTCAAACA TGTTT Pro Ala Phe Leu Tyr Lys Val Val
 Green Fluorescent Protein (cycle-3 GFP)
 3177 GAT CTA GAG GGC CCC GCG GCT AGC AAA GGA GAA GAA CTT TTC ACT GGA GGT GTC CCA
 Asp Leu Glu Gly Pro Ala Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 3234 ATT CTT GTT GAA TTA GAT GGT GAT GTT AAT GGG CAC AAA TTT TCT GTC AGT GGA GAG
 Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 GFP reverse priming site
 3291 GGT GAA GGT GAT GCT ACA TAC GGA AAG CTT ACC CTT AAA TTT ATT TGC ACT ACT GGA
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
 3348 AAA CTA CCT GTT ...
 Lys Leu Pro Val ...

FIG. 62

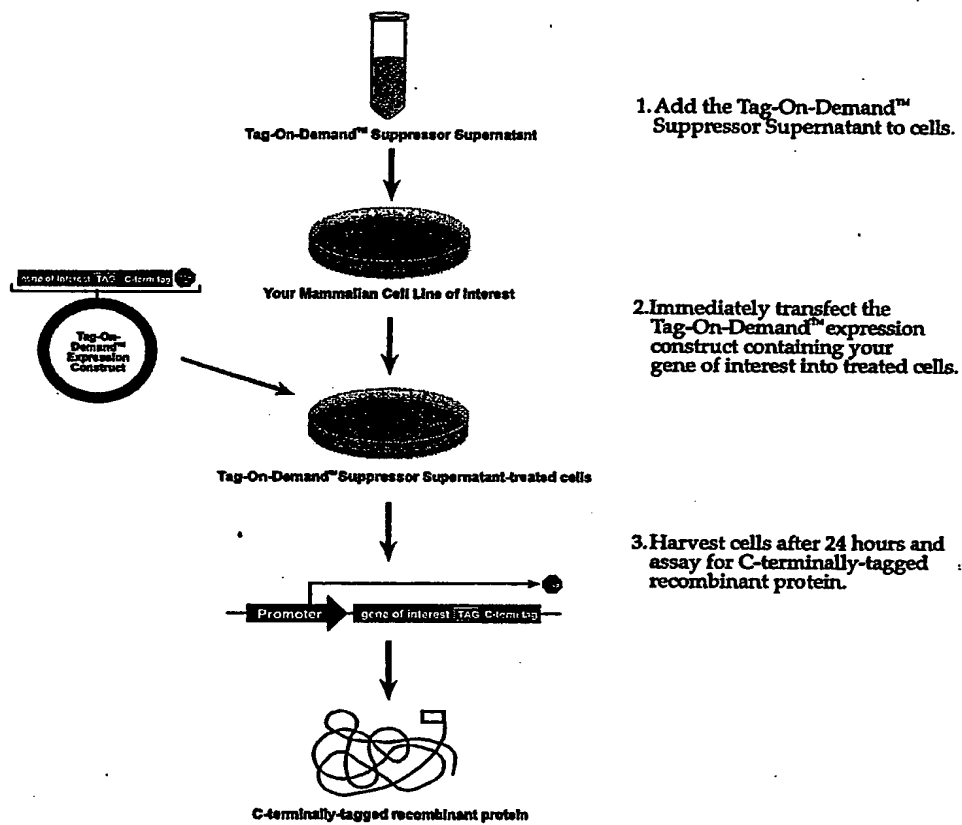


FIG. 63

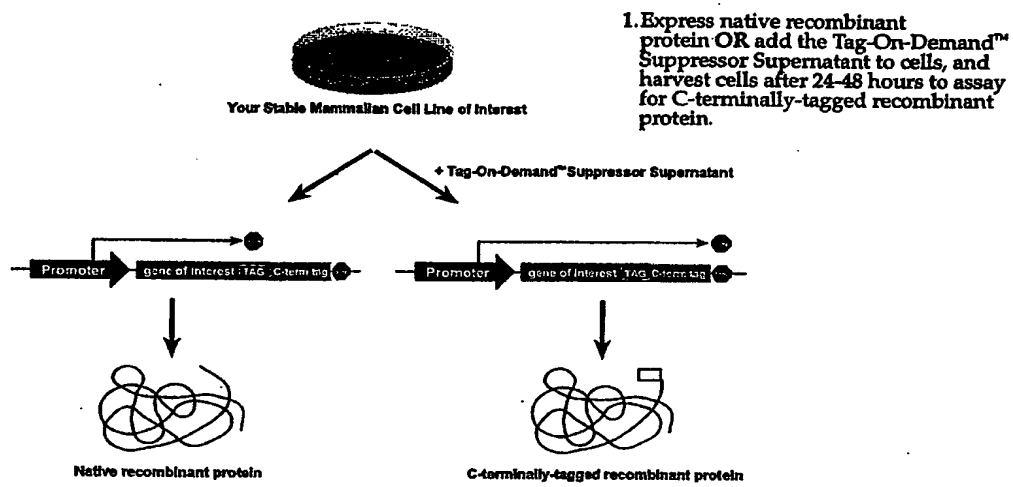
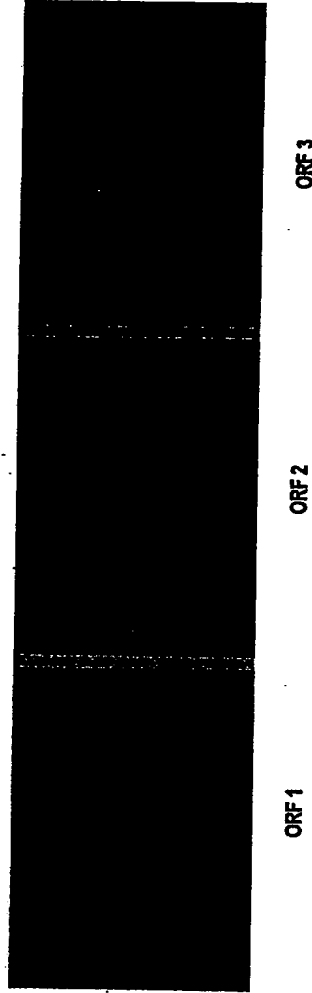


FIG. 64



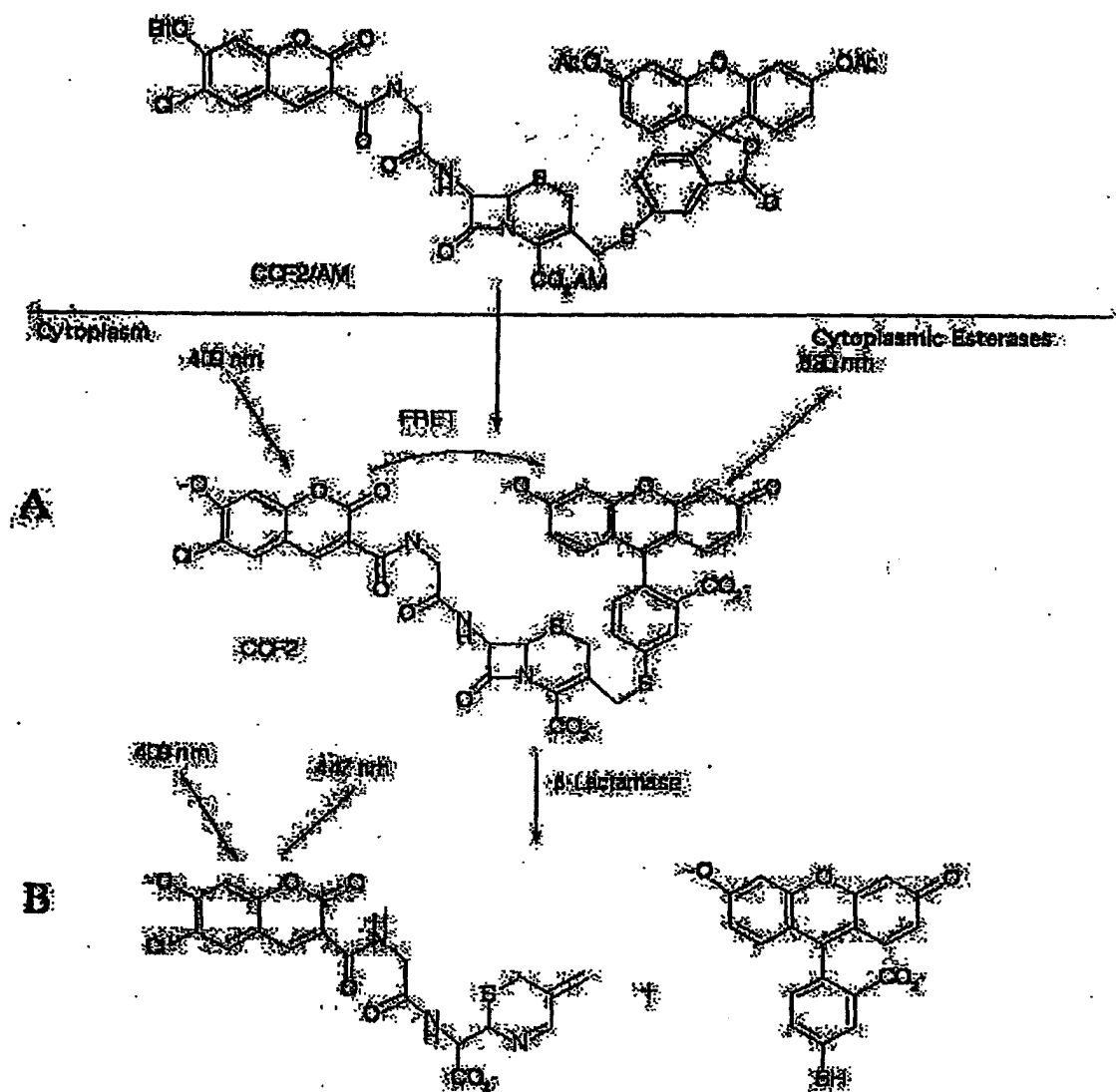


FIG. 65

Fig. 66

Sequential method



Simultaneous method



Fluorescent

Brightfield

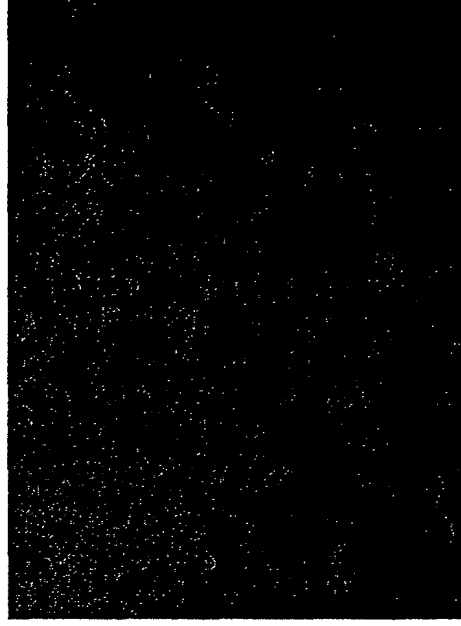
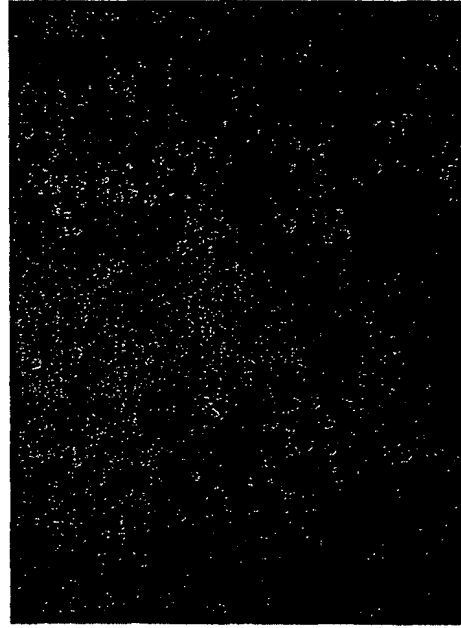
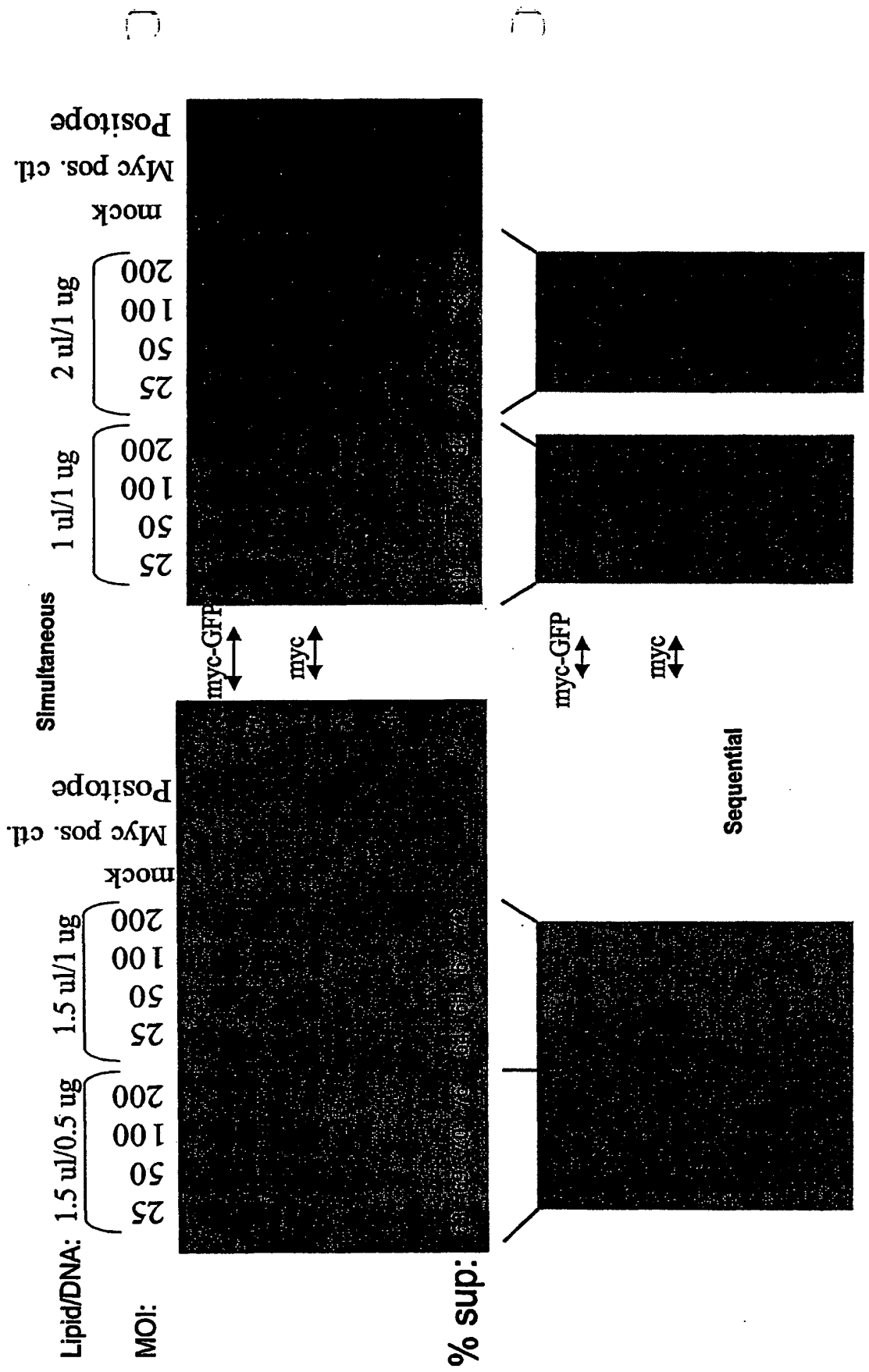


FIG. 67



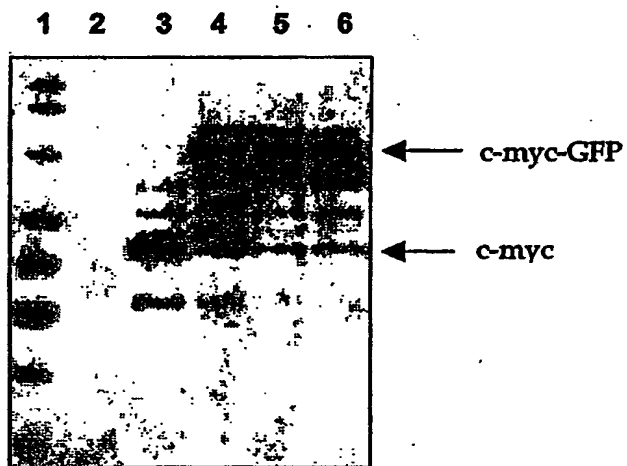


Fig. 6b

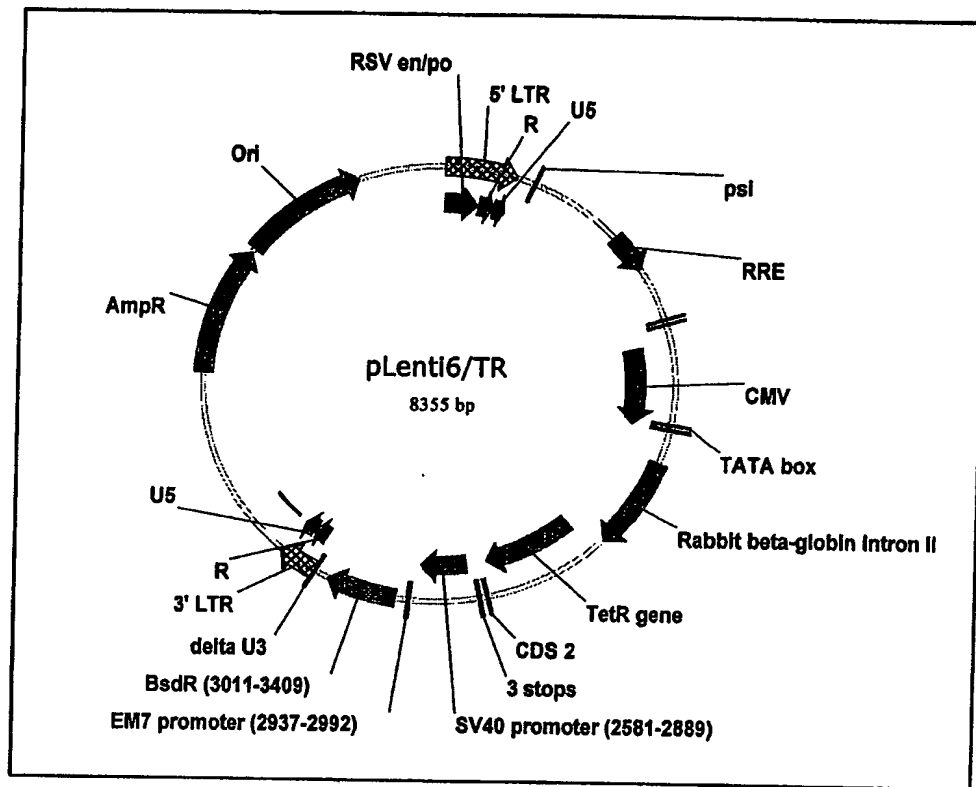


FIG. 69

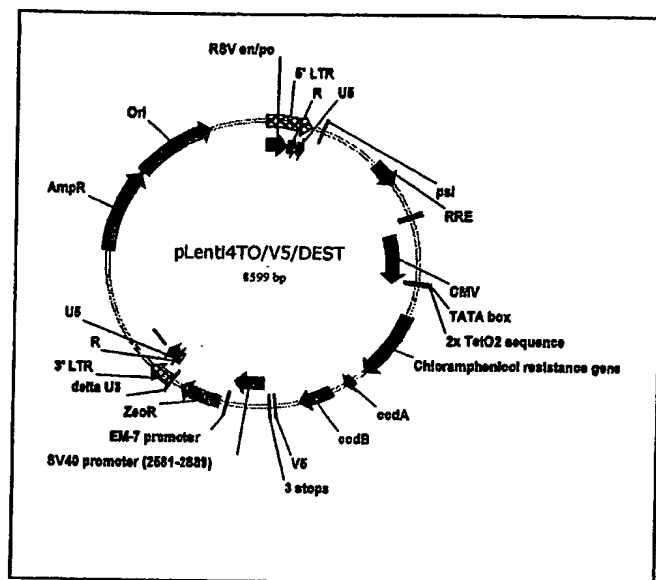


FIG. 70A

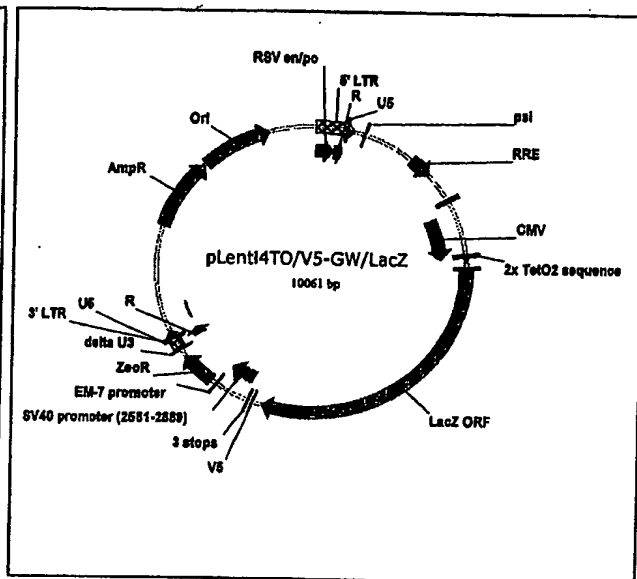


FIG. 70B

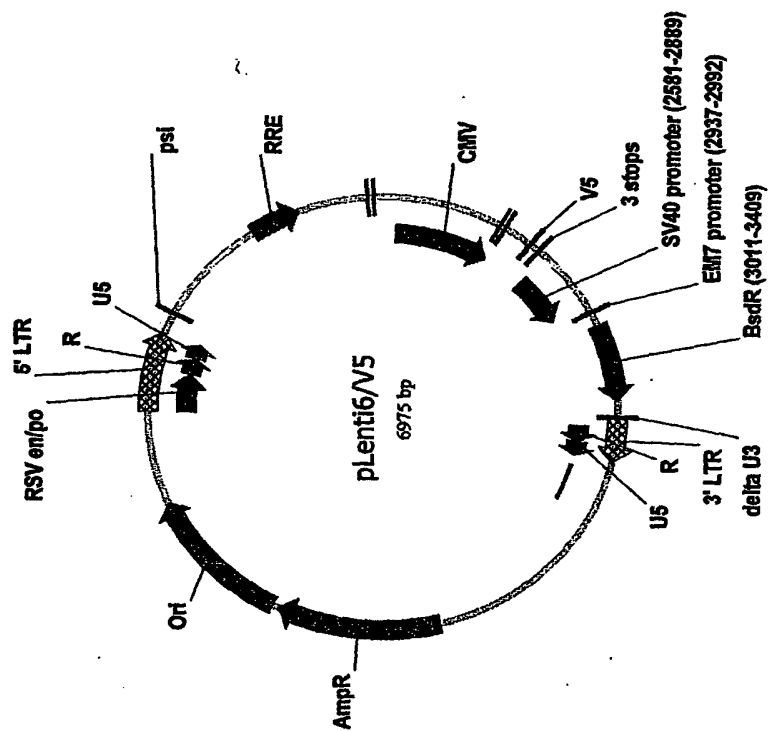


FIG. 71

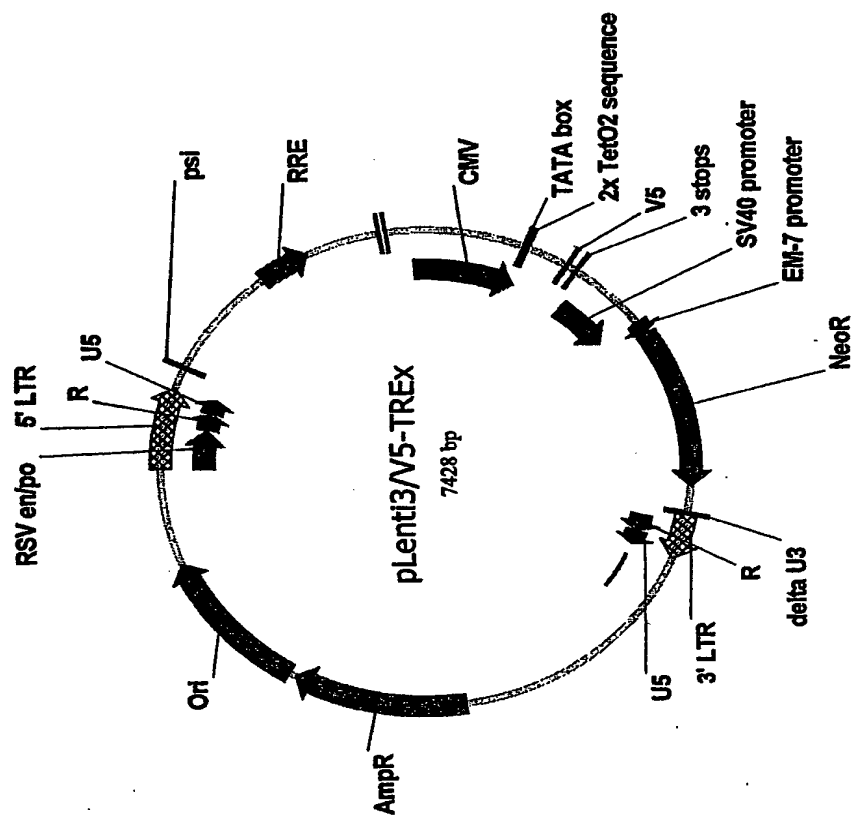


FIG. 72

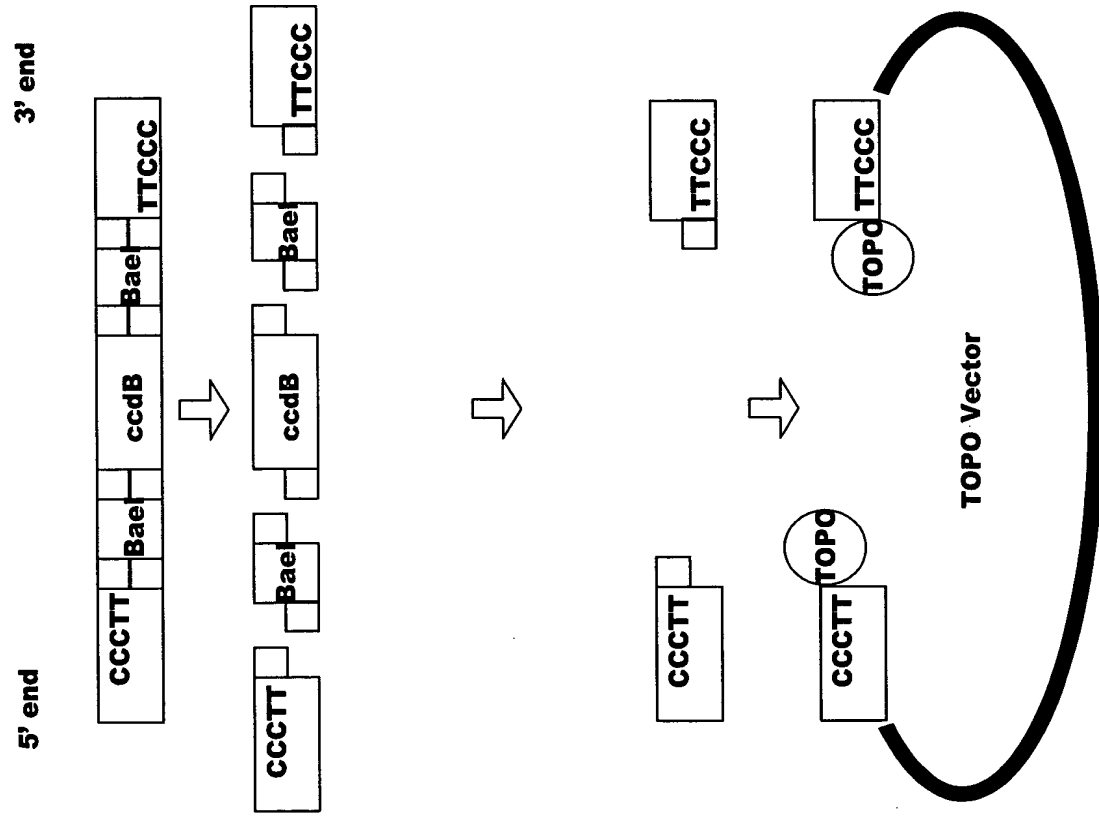


FIG. 73